

FORM PTO-1390
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1781

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

09/673840

INTERNATIONAL APPLICATION NO

PCT/DE99/01163

INTERNATIONAL FILING DATE

15 April 1999

PRIORITY DATE CLAIMED

21 April 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BLADDER TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

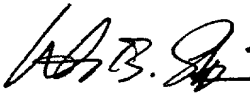
1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☐ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☐ A copy of the International Search Report (PCT/ISA/210).
8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
10. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

Items 13. to 19. below concern document(s) or information included:

13. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included
15. ☐ A FIRST preliminary amendment.
- ☐ A SECOND or SUBSEQUENT preliminary amendment.
16. ☐ A substitute specification.
17. ☐ A change of power of attorney and/or address letter.
18. ☐ Certificate of Mailing by Express Mail
19. ☒ Other items or information:

Sequence Listing with disk

COPY

U.S. APPLICATION NO. (if known) 09/673840		INTERNATIONAL APPLICATION NO PCT/DE99/01163		ATTORNEY'S DOCKET NUMBER SCH 1781	
17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)): Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$1,000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100 00 <div style="text-align: right;">ENTER APPROPRIATE BASIC FEE AMOUNT = \$860.00</div>				CALCULATIONS PTO USE ONLY	
Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				\$0.00	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	- 20 =	0	x \$ 18.00	\$0.00	
Independent claims	- 3 =	0	x \$ 80.00	\$0.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00		
TOTAL OF ABOVE CALCULATIONS =				\$860.00	
Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
SUBTOTAL =				\$0.00	
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
TOTAL NATIONAL FEE =				\$860.00	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
TOTAL FEES ENCLOSED =				\$860.00	
				Amount to be refunded:	
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a. <input checked="" type="checkbox"/> A check in the amount of <u>\$860.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: October 23, 2000 AJZ(HBS): jmm k:\pat\sch\1781\natl phase transmtl				 SIGNATURE Harry B. Shubin NAME <u>32,004</u> REGISTRATION NUMBER	

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

International Application No. : PCT/DE99/01163
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U.S. Serial No. : 09/673,840
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Applicant(s) : SPECHT, Thomas, et al.
Title: HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.
4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.
5. (Amended) A nucleic acid sequence according to claim 1, wherein it has 90% homology to a human nucleic acid sequence.
6. (Amended) A nucleic acid sequence according to claim 1, wherein it has 95% homology to a human nucleic acid sequence.
7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim 1, in such a sufficient amount that they hybridize with the sequences according to claim 1.

8. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to claim 1, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 1, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to claim 11, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to claim 1 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to claim 1.

18. (Amended) Host cell according to claim 16, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to claim 16 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to claim 1, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to claim 1, wherein it is an mRNA sequence.

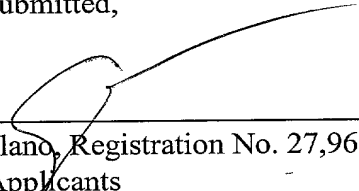
35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 300 to 3500 bp.

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



Anthony J. Zelano, Registration No. 27,969
Attorney for Applicants
MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
Arlington Courthouse Plaza I
2200 Clarendon Boulevard, Suite 1400
Arlington, Virginia 22201
Direct Dial: 703-812-5311
Facsimile: 703-243-6410
Internet Address: zelano@mwzb.com

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 3-11, 13-14, 16, 18-19, 27-35 and 38 have been amended as follows:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.

4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.

5. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 4~~, wherein it has 90% homology to a human nucleic acid sequence.

6. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 4~~, wherein it has %95% homology to a human nucleic acid sequence.

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in ~~claims~~claim 1 ~~to 6~~, in such a sufficient amount that they hybridize with the sequences according to ~~claims~~claim 1 ~~to 6~~.

8. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 7~~, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 7~~, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to ~~one of claims~~claim 1 ~~to 9~~, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to ~~one of claims~~claim 1 ~~to 9~~, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to ~~one of claims~~claim 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to ~~claims~~claim 1 to 10 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to ~~one of claims~~claim 1 to 10.

18. (Amended) Host cell according to ~~one of claims~~claim 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to ~~claims~~claim 16 to 18 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 10~~, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 10~~, wherein it is an mRNA sequence.

35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to ~~claims~~claim 1 ~~to 7~~, wherein the size of the fragment has a length of at least 300 to 3500 bp.

Human Nucleic Acid Sequences from Normal Bladder Tissue

The invention relates to human nucleic acid sequences from normal bladder tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer is the bladder tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

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A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which play a role as candidate genes in the bladder tumor, have now been found.

Nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 or a complementary or

allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which are expressed elevated in the normal bladder tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-127 and 391-403.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-127 and 391-403 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic,

such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 128-390 and 404-431.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq ID Nos. 128-390 and 404-431 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 128-390 and 404-431 according to the invention can also be used as tools for finding active ingredients against the bladder tumor, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides, which can be used as tools for finding active ingredients against the bladder tumor.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in the gene therapy for treatment of bladder tumors or for the production of a pharmaceutical agent for treatment of bladder tumors.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained

from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-127 and 391-403, genomic BAC-, PAC- and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for Tumor-related Candidate Genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the bladder tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2

Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1 Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 1 was found, which occurs 12.2 x more strongly in the normal bladder tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0026	12.203	0.0819
Breast	0.0064	0.0056	1.1342	0.8817
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0060	0.0156	0.3838	2.6058
Endocrine tissue	0.0068	0.0201	0.3396	2.9444
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0111	0.0226	0.4909	2.0372
Hematopoietic	0.0107	0.0379	0.2823	3.5422
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0234	0.7380	1.3551
Lung	0.0083	0.0184	0.4516	2.2144
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0081	0.0274	0.2974	3.3626
Pancreas	0.0083	0.0110	0.7479	1.3371
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0204	0.7482	1.3366
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0139			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0051
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0157	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0107	Skin-muscle	0.0065
Suprarenal gland	0.0253	Testicles	0.0077
Kidney	0.0507	Lung	0.0082
Placenta	0.0000	Nerves	0.0090
Prostate	0.0182	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0377	Uterus_n	0.0042

In an analogous procedure, the following Northern blots were also found:

Electronic Northern for SEQ. ID NO.: 2

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0741	0.0102	7.2459	0.1380
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0061	0.8467	1.1810
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0109	0.0064	1.7060	0.5862
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0052			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0585	0.0153	3.8136	0.2622
Breast	0.0064	0.0000	undef	0.0000
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0204	0.0100	2.0377	0.4907
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0059	0.0092	0.6400	1.5626
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0104	0.0020	5.0803	0.1968
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0654	0.0362	1.8064	0.5536
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0000	0.1908	0.0000	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0803			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0333

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0351	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 6					
	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T	T/N	
Bladder	0.0390	0.0026	15.2544	0.0656	
Breast	0.0460	0.0056	8.1663	0.1225	
Small intestine	0.0123	0.0331	0.3707	2.6973	
Ovary	0.0000	0.0052	0.0000	undef	
Endocrine tissue	0.0119	0.0050	2.3774	0.4206	
Gastrointestinal	0.0038	0.0000	undef	0.0000	
Brain	0.0052	0.0072	0.7200	1.3890	
Hematopoietic	0.0013	0.0000	undef	0.0000	
Skin	0.0294	0.0000	undef	0.0000	
Hepatic	0.0143	0.0065	2.2059	0.4533	
Heart	0.0074	0.0000	undef	0.0000	
Testicles	0.0058	0.0117	0.4920	2.0326	
Lung	0.0021	0.0000	undef	0.0000	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0103	0.0240	0.4283	2.3347	
Kidney	0.0516	0.0000	undef	0.0000	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0090	0.0000	undef	0.0000	
Prostate	0.0044	0.0064	0.6824	1.4654	
Uterus-endometrium	0.0270	0.0000	undef	0.0000	
Uterus-myometrium	0.0381	0.0000	undef	0.0000	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.1087				
Prostate hyperplasia	0.0059				
Seminal vesicle	0.0089				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix	0.0319				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0272
Gastrointestinal	0.0557	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0498	Skin-muscle	0.0194
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0151
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 7

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0026	13.7290	0.0728
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0044	0.0000	undef	0.0000
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0063
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0040
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

TABLE 1 "TABLE 1" 1988

Electronic Northern for SEQ. ID NO.: 8

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0051	0.4320	2.3149
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0139	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0273	0.0026	10.6781	0.0936
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8686
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0037	0.0051	0.7200	1.3890
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0060	0.8567	1.1673
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0000	0.0085	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0052			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 12

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0858	0.0358	2.3971	0.4172
Breast	0.0435	0.0338	1.2854	0.7779
Small intestine	0.0276	0.0165	1.6683	0.5994
Ovary	0.0120	0.0182	0.6579	1.5201
Endocrine tissue	0.0290	0.0176	1.6496	0.6062
Gastrointestinal	0.0594	0.0231	2.5679	0.3894
Brain	0.0333	0.0657	0.5062	1.9754
Hematopoietic	0.0134	0.0000	undef	0.0000
Skin	0.0514	0.0000	undef	0.0000
Hepatic	0.0381	0.0129	2.9412	0.3400
Heart	0.0413	0.0275	1.5034	0.6652
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0384	0.0164	2.3497	0.4256
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0188	0.0360	0.5235	1.9102
Kidney	0.0217	0.0548	0.3965	2.5219
Pancreas	0.0132	0.0166	0.7977	1.2536
Penis	0.0779	0.0000	undef	0.0000
Prostate	0.0632	0.0447	1.4136	0.7074
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0416			
Prostate hyperplasia	0.0595			
Seminal vesicle	0.0712			
Sensory organs	0.0118			
White blood cells	0.0087			
Cervix	0.0426			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.1293
Gastrointestinal	0.0250	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0118	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0338
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.1014	Testicles	0.0000
Kidney	0.0185	Lung	0.0301
Placenta	0.0242	Nerves	0.0410
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0628	Sensory Organs	0.0624
		Uterus_n	

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0468	0.0077	6.1018	0.1639
Breast	0.0294	0.0075	3.9130	0.2556
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0192	0.0000	undef	0.0000
Brain	0.0059	0.0062	0.9599	1.0417
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0808	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0540	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0156	0.0082	1.9051	0.5249
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.1216	0.0000	undef	0.0000
Kidney	0.0000	0.0274	0.0000	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.1587	0.0000	undef	0.0000
Prostate	0.0087	0.0106	0.8189	1.2211
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0272	1.6834	0.5940
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0426			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0249	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0309
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0090
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus n	0.0208

Electronic Northern for SEQ. ID NO.: 14

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0026	13.7290	0.0728
Breast	0.0102	0.0075	1.3611	0.7347
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0090	0.0026	3.4538	0.2895
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0233	0.0137	1.6961	0.5896
Testicles	0.0000	0.0000	undef	undef
Lung	0.0135	0.0041	3.3022	0.3028
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0634	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0359	0.0000	undef	0.0000
Prostate	0.0218	0.0043	5.1181	0.1954
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
% frequency	% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0062	Lung	0.0181
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0583
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 17

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0026	10.6781	0.0936
Breast	0.0307	0.0038	8.1663	0.1225
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0249	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0020	3.0482	0.3281
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0274	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0087	0.0000	undef	0.0000
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0288			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0106			

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 18

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0585	0.0230	2.5424	0.3933
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0368	0.0165	2.2244	0.4496
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0115	0.0046	2.4850	0.4024
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0509	0.0000	undef	0.0000
Prostate	0.0218	0.0149	1.4623	0.6838
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0543	0.4208	2.3761
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0429	0.0153	2.7966	0.3576
Breast	0.0141	0.0282	0.4991	2.0038
Small intestine	0.0307	0.0165	1.8537	0.5395
Ovary	0.0300	0.0390	0.7675	1.3029
Endocrine tissue	0.0409	0.0176	2.3288	0.4294
Gastrointestinal	0.0230	0.0139	1.6567	0.6036
Brain	0.0200	0.0298	0.6703	1.4919
Hematopoietic	0.0160	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0143	0.0259	0.5515	1.8133
Heart	0.0339	0.0000	undef	0.0000
Testicles	0.0288	0.0234	1.2299	0.8130
Lung	0.0270	0.0409	0.6604	1.5141
Stomach-esophagus	0.0483	0.0230	2.1009	0.4760
Muscle-skeleton	0.0394	0.0240	1.6419	0.6090
Kidney	0.0244	0.0205	1.1896	0.8406
Pancreas	0.0198	0.0276	0.7180	1.3928
Penis	0.0359	0.0533	0.6739	1.4839
Prostate	0.0305	0.0255	1.1942	0.8374
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0534	0.0272	1.9640	0.5092
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0595			
Seminal vesicle	0.0267			
Sensory organs	0.0118			
Sensory organs	0.0286			
White blood cells	0.0426			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0222	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0285	Hematopoietic	0.0000
Lung	0.0470	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0247	Lung	0.0082
Placenta	0.0121	Nerves	0.0080
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus n	0.0250

Electronic Northern for SEQ. ID NO.: 21

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0150	0.2264	4.4166
Gastrointestinal	0.0000	0.0139	0.0000	undef
Brain	0.0177	0.0031	5.7597	0.1736
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 23

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0390	0.0000	undef	0.0000
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0115	0.0046	2.4850	0.4024
Brain	0.0022	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0065	0.0064	1.0236	0.9769
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0475	0.4810	2.0791
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0267			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0051	6.8645	0.1457
Breast	0.0026	0.0056	0.4537	2.2042
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0090	0.0130	0.6908	1.4477
Endocrine tissue	0.0068	0.0075	0.9057	1.1042
Gastrointestinal	0.0172	0.0139	1.2425	0.8048
Brain	0.0044	0.0082	0.5400	1.8520
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0042	0.0143	0.2903	3.4446
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0000	0.0205	0.0000	undef
Pancreas	0.0033	0.0110	0.2991	3.3428
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0087	0.0128	0.6824	1.4654
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0181
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0254	Testicles	0.0154
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0416

Electronic Northern for SEQ. ID NO.: 25

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 26

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0429	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0012
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 27

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0000	undef	0.0000
Breast	0.0090	0.0056	1.5879	0.6298
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8686
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0030	0.0051	0.5760	1.7362
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0064
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 29

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0051	6.1018	0.1639
Breast	0.0307	0.0019	16.3327	0.0612
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0120	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0015	0.0062	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0138	0.0412	0.3341	2.9932
Testicles	0.0403	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0274	0.0300	0.9138	1.0944
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0050	0.0331	0.1496	6.6857
Penis	0.0359	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0686	0.0679	1.0100	0.9901
Uterus-general	0.0458	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0213			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0036	Testicles	0.0077
Kidney	0.0000	Lung	0.0410
Placenta	0.0124	Nerves	0.0010
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0250

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Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0021	1.0236	0.9769
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0499	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 32				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0026	9.1527	0.1093
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0068
Prostate	0.0000	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 33				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0085	0.0150	0.5660	1.7667
Gastrointestinal	0.0019	0.0139	0.1381	7.2434
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0109	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0070
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 34

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 35

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0310
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 36				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 37

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0089	0.0144	0.6171	1.6205
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0135	0.0123	1.1007	0.9085
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0034	0.0120	0.2856	3.5020
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0149	0.1462	6.8384
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0255	0.1908	0.1334	7.4943
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0104			
Cervix	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development 0.0000
Gastrointestinal 0.0056
Brain 0.0000
Hematopoietic 0.0118
Skin 0.0000
Hepatic 0.0000
Heart-blood vessels 0.0036
Lung 0.0108
Suprarenal gland 0.0000
Kidney 0.0062
Placenta 0.0000
Prostate 0.0000
Sensory organs 0.0000

Breast 0.0000
Ovary_n 0.1595
Ovary_t 0.0253
Endocrine tissue 0.0000
Fetal 0.0116
Gastrointestinal 0.0366
Hematopoietic 0.0456
Skin-muscle 0.0162
Testicles 0.0000
Lung 0.0000
Nerves 0.0221
Prostate 0.0068
Sensory Organs 0.0077
Uterus_n 0.0000

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Electronic Northern for SEQ. ID NO.: 38

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0051	5.3391	0.1873
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0081	0.0031	2.6399	0.3788
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0136	0.0205	0.6609	1.5132
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0109	0.0021	5.1181	0.1954
Uterus-endometrium	0.0068	0.0528	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0128	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0125
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Suprarenal gland	0.0507
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0164
Lung	0.0070
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 39				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

Electronic Northern for SEQ. ID NO.: 40

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

"0000" 0000 0000 0000

Electronic Northern for SEQ. ID NO.: 43

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0041	1.2701	0.7873
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 44

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	FETUS	% frequency	
	% frequency		
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

"0000" 0000 0000

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 47

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

"BDEB" DBE4353

Electronic Northern for SEQ. ID NO.: 48

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	FETUS	% frequency	
	% frequency		
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0060
Placenta	0.0061	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

"1992" 0402/950

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 51

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0136	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0166	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 52

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 53				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 54

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0057
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 55

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 56		NORMAL		TUMOR		Ratios	
	% frequency	% frequency	% frequency	N/T	T/N		
Bladder	0.0156	0.0000	undef	0.0000			
Breast	0.0026	0.0000	undef	0.0000			
Small intestine	0.0000	0.0000	undef	undef			
Ovary	0.0030	0.0000	undef	0.0000			
Endocrine tissue	0.0051	0.0000	undef	0.0000			
Gastrointestinal	0.0038	0.0093	0.4142	2.4145			
Brain	0.0000	0.0000	undef	undef			
Hematopoietic	0.0000	0.0000	undef	undef			
Skin	0.0037	0.0000	undef	0.0000			
Hepatic	0.0000	0.0000	undef	undef			
Heart	0.0011	0.0000	undef	0.0000			
Testicles	0.0000	0.0000	undef	undef			
Lung	0.0010	0.0020	0.5080	1.9684			
Stomach-esophagus	0.0000	0.0000	undef	undef			
Muscle-skeleton	0.0017	0.0000	undef	0.0000			
Kidney	0.0054	0.0068	0.7930	1.2610			
Pancreas	0.0000	0.0000	undef	undef			
Penis	0.0000	0.0000	undef	undef			
Prostate	0.0022	0.0043	0.5118	1.9538			
Uterus-endometrium	0.0000	0.0000	undef	undef			
Uterus-myometrium	0.0000	0.0000	undef	undef			
Uterus-general	0.0000	0.0000	undef	undef			
Breast hyperplasia	0.0030						
Prostate hyperplasia	0.0000						
Seminal vesicle	0.0000						
Sensory organs	0.0009						
White blood cells	0.0000						
Cervix							

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 57

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0058	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 58

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0026	9.1527	0.1093
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 59

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0000	0.0020	0.0000	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 60

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
% frequency	% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 61				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 62

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 63

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0051	6.8645	0.1457
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0106			
Cervix				

		STANDARDIZED/SUBTRACTED	
	FETUS	LIBRARIES	
	% frequency	% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0050
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

"ENSED" DATA

Electronic Northern for SEQ. ID NO.: 65

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED	
		% frequency	LIBRARIES	
			% frequency	
Development	0.0000	Breast	0.0000	
Gastrointestinal	0.0000	Ovary_n	0.0000	
Brain	0.0000	Ovary_t	0.0000	
Hematopoietic	0.0000	Endocrine tissue	0.0000	
Skin	0.0000	Fetal	0.0000	
Hepatic	0.0000	Gastrointestinal	0.0000	
Heart-blood vessels	0.0000	Hematopoietic	0.0000	
Lung	0.0000	Skin-muscle	0.0000	
Suprarenal gland	0.0000	Testicles	0.0000	
Kidney	0.0000	Lung	0.0000	
Placenta	0.0000	Nerves	0.0000	
Prostate	0.0000	Prostate	0.0077	
Sensory organs	0.0000	Sensory Organs	0.0000	
		Uterus_n		

Electronic Northern for SEQ. ID NO.: 67				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0390	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000		0.0245
Hepatic	0.0000	Fetal	0.0000
Heart-blood vessels	0.0000	Gastrointestinal	0.0000
Lung	0.0036	Hematopoietic	0.0057
Suprarenal gland	0.0000	Skin-muscle	0.0000
Kidney	0.0000	Testicles	0.0000
Placenta	0.0000	Lung	0.0000
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 69				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0128
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0462	Skin-muscle	0.0227
Suprarenal gland	0.0036	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0171
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 72

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0585	0.0077	7.6272	0.1311
Breast	0.0192	0.0019	10.2079	0.0980
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0307	0.0000	undef	0.0000
Brain	0.0118	0.0062	1.9199	0.5209
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0190	0.0065	2.9412	0.3400
Heart	0.0244	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0509	0.0000	undef	0.0000
Prostate	0.0153	0.0085	1.7913	0.5582
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0320			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development
Gastrointestinal
Brain
Hematopoietic
Skin
Hepatic
Heart-blood vessels
Lung
Suprarenal gland
Kidney
Placenta
Prostate
Sensory organs

0.0000
0.0167
0.0000
0.0000
0.0000
0.0000
0.0071
0.0036
0.0000
0.0000
0.0061
0.0000
0.0251

Breast
Ovary_n
Ovary_t
Endocrine tissue
Fetal
Gastrointestinal
Hematopoietic
Skin-muscle
Testicles
Lung
Nerves
Prostate
Sensory Organs
Uterus_n

0.0204
0.0000
0.0101
0.0000
0.0082
0.0000
0.0162
0.0000
0.0082
0.0040
0.0068
0.0155
0.0000

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Electronic Northern for SEQ. ID NO.: 73

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 75

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

"FETUS" DATA

Electronic Northern for SEQ. ID NO.: 77				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0051	6.8645	0.1457
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0067	0.0010	6.4796	0.1543
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0087
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0000	Lung	0.0090
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0458
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0412	0.0257	38.9118
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 79

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 80

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0624	0.0102	6.1018	0.1639
Breast	0.0141	0.0056	2.4953	0.4008
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0150	0.0078	1.9188	0.5212
Endocrine tissue	0.0187	0.0050	3.7359	0.2677
Gastrointestinal	0.0307	0.0139	2.2089	0.4527
Brain	0.0214	0.0082	2.6099	0.3832
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0190	0.0065	2.9412	0.3400
Heart	0.0360	0.0137	2.6213	0.3815
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0041	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0171	0.0060	2.8555	0.3502
Kidney	0.0136	0.0548	0.2478	4.0351
Pancreas	0.0083	0.0387	0.2137	4.6800
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0064	1.3648	0.7327
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0288			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.1246			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0205
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 82

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0390	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 83

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0026	10.6781	0.0936
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0229	0.0031	7.4396	0.1344
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0253
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0201
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0310
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 85

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

		FETUS	STANDARDIZED/SUBTRACTED	
		% frequency	LIBRARIES	
			% frequency	
Development	0.0000	Breast	0.0000	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000	0.0000
Brain	0.0000	Ovary_t	0.0000	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000	0.0000
Skin	0.0000	Fetal	0.0000	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000	0.0000
Lung	0.0000	Skin-muscle	0.0000	0.0000
Suprarenal gland	0.0000	Testicles	0.0000	0.0000
Kidney	0.0000	Lung	0.0000	0.0000
Placenta	0.0000	Nerves	0.0000	0.0000
Prostate	0.0000	Prostate	0.0000	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000	0.0000
		Uterus_n		

TABLE 1

Electronic Northern for SEQ. ID NO.: 86

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0051	5.3391	0.1873
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 88

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0386
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 90				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0312	0.0051	6.1018	0.1639
Small intestine	0.0102	0.0113	0.9074	1.1021
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0051	0.0125	0.4075	2.4537
Brain	0.0077	0.0000	undef	0.0000
Hematopoietic	0.0067	0.0329	0.2025	4.9386
Skin	0.0080	0.0000	undef	0.0000
Hepatic	0.0330	0.0000	undef	0.0000
Heart	0.0333	0.0323	1.0294	0.9714
Testicles	0.0127	0.0137	0.9252	1.0809
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0156	0.0082	1.9051	0.5249
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0051	0.0120	0.4283	2.3347
Pancreas	0.0027	0.0205	0.1322	7.5658
Penis	0.0050	0.0110	0.4487	2.2286
Prostate	0.0060	0.0267	0.2246	4.4517
Uterus-endometrium	0.0131	0.0128	1.0236	0.9769
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0208			
Sensory organs	0.0089			
White blood cells	0.0118			
Cervix	0.0147			
	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0608
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0198
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0545	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0697
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 93

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0166	0.0226	0.7372	1.3564
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0270	0.0000	undef	0.0000
Endocrine tissue	0.0238	0.0276	0.8645	1.1567
Gastrointestinal	0.0115	0.0093	1.2425	0.8048
Brain	0.0089	0.0072	1.2342	0.8102
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0230	0.0117	1.9679	0.5082
Lung	0.0218	0.0266	0.8207	1.2185
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0149	0.0221	0.6731	1.4857
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0240	0.0213	1.1260	0.8881
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0340	0.6734	1.4851
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0445			
Sensory organs	0.0235			
White blood cells	0.0009			
Cervix	0.0213			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

"9999" 0.0000 0.0000

Electronic Northern for SEQ. ID NO.: 94

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0026	7.6272	0.1311
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0119	0.0150	0.7925	1.2619
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0103	0.2880	3.4724
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0709
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0185	Lung	0.0010
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0250
		Uterus_n	

"BBB" "BBB" "BBB"

Electronic Northern for SEQ. ID NO.: 95

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0026	13.7290	0.0728
Breast	0.0026	0.0094	0.2722	3.6736
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0037	0.0051	0.7200	1.3890
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0190	0.0129	1.4706	0.6800
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0050	0.0166	0.2991	3.3428
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0000			
Cervix				

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0155
		Uterus_n	0.0208

"FETUS" 04024953

Electronic Northern for SEQ. ID NO.: 96

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0090	0.0094	0.9527	1.0496
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0153	0.0176	0.8733	1.1451
Gastrointestinal	0.0096	0.0185	0.5177	1.9316
Brain	0.0081	0.0031	2.6399	0.3788
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0135	0.0528	0.2561	3.9053
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0324
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0328
Placenta	0.0061	Nerves	0.0141
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 97

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0064	0.0038	1.7013	0.5878
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0156	0.1919	5.2117
Endocrine tissue	0.0136	0.0251	0.5434	1.8403
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0074	0.0277	0.2667	3.7502
Hematopoietic	0.0134	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0127	0.0412	0.3084	3.2426
Testicles	0.0115	0.0585	0.1968	5.0816
Lung	0.0104	0.0204	0.5080	1.9684
Stomach-esophagus	0.0193	0.0230	0.8404	1.1900
Muscle-skeleton	0.0120	0.0240	0.4997	2.0011
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0083	0.0331	0.2493	4.0114
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0240	0.0277	0.8661	1.1545
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0113			
Cervix	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0181
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0082
Nerves	0.0070
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 98

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0113	0.2268	4.4083
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0229	0.0062	3.7198	0.2688
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0847	0.0000	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0106			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0557	Breast	0.0068
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0175
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0389
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0000	Nerves	0.0251
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0310
		Uterus_n	0.0208

009923 01924955

Electronic Northern for SEQ. ID NO.: 99				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0026	12.2035	0.0819
Breast	0.0166	0.0132	1.2638	0.7912
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0090	0.0026	3.4538	0.2895
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0115	0.0231	0.4970	2.0121
Brain	0.0074	0.0082	0.8999	1.1112
Hematopoietic	0.0120	0.0379	0.3176	3.1487
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0275	0.3084	3.2426
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0104	0.0061	1.6934	0.5905
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0109	0.0274	0.3965	2.5219
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0150	0.0000	undef	0.0000
Penis	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0113			
Cervix	0.0106			

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0036
Suprarenal gland	0.0507
Kidney	0.0247
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0050
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0000
Lung	0.0000
Nerves	0.0040
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 100

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0156	0.0000	undef	0.0000
Small intestine	0.0051	0.0056	0.9074	1.1021
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0026	1.1513	0.8686
Gastrointestinal	0.0000	0.0075	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0030	0.0051	0.5760	1.7362
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0137	0.1542	6.4853
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0052	0.0041	1.2701	0.7873
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0000	0.0055	0.0000	undef
Prostate	0.0060	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0136	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0061			
	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0125

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0026	9.1527	0.1093
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0015	0.0021	0.7200	1.3890
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0150	0.0800	0.1872	5.3421
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0078			
Cervix	0.0213			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0408
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0092
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0065	0.0021	3.0709	0.3256
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 104

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0051	6.1018	0.1639
Breast	0.0102	0.0056	1.8147	0.5510
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0130	0.0104	1.7269	0.5791
Endocrine tissue	0.0085	0.0176	0.4852	2.0611
Gastrointestinal	0.0172	0.0046	3.7275	0.2683
Brain	0.0126	0.0123	1.0199	0.9804
Hematopoietic	0.0040	0.0758	0.0529	18.8919
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0138	0.0275	0.5011	1.9955
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0145	0.0102	1.4225	0.7030
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0206	0.0000	undef	0.0000
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0050	0.0110	0.4487	2.2286
Penis	0.0130	0.0000	undef	0.0000
Prostate	0.0087	0.0000	undef	0.0000
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0136	1.1223	0.8911
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0353			
White blood cells	0.0043			
Cervix	0.0000			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0185
Placenta	0.1030
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0204
Ovary_n	0.1595
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0192
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0324
Testicles	0.0154
Lung	0.0000
Nerves	0.0151
Prostate	0.0000
Sensory Organs	0.0077
Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 105

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0115	0.0132	0.8750	1.1429
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0030	0.0041	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0319			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0259
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0100
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 106

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0077	4.0678	0.2458
Breast	0.0192	0.0019	10.2079	0.0980
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0068	0.0075	0.9057	1.1042
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0118	0.0164	0.7200	1.3890
Hematopoietic	0.0080	0.0379	0.2117	4.7230
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0191	0.0275	0.6939	1.4412
Testicles	0.0000	0.0000	undef	undef
Lung	0.0239	0.0102	2.3370	0.4279
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0051	0.0240	0.2142	4.6693
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0033	0.0110	0.2991	3.3428
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0204	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0320			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0118			
White blood cells	0.0087			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0198
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0213	Hematopoietic	0.0171
Lung	0.0181	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0121	Nerves	0.0161
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.2762	Sensory Organs	0.0000
		Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 107

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 108

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0022	0.0103	0.2160	4.6299
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0061	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0137	0.0000	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0095			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0759
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0274
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0507	0.0179	2.8330	0.3530
Breast	0.0153	0.0000	undef	0.0000
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0270	0.0000	undef	0.0000
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0044	0.0010	4.3198	0.2315
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0073	0.0000	undef	0.0000
Stomach-esophagus	0.0580	0.0230	2.5211	0.3967
Muscle-skeleton	0.0771	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0033	0.0221	0.1496	6.6857
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0174	0.0106	1.6378	0.6106
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0534			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0816
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0242	Nerves	0.0030
Prostate	0.0748	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 110

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0230	0.0038	6.1248	0.1633
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0120	0.0000	undef	0.0000
Endocrine tissue	0.0136	0.0025	5.4340	0.1840
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0194	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0212	0.0137	1.5420	0.6485
Testicles	0.0000	0.0000	undef	undef
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0180	0.3807	2.6265
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0068	4.4891	0.2228
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix	0.0532			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0417	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0080
Placenta	0.0121	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 111

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0026	12.2035	0.0819
Breast	0.0051	0.0019	2.7221	0.3674
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0041	0.5400	1.8520
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0124	Lung	0.0082
Placenta	0.0121	Nerves	0.0020
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 112				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0021	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0043			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0063
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0032
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 113

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0026	12.2035	0.0819
Breast	0.0102	0.0019	5.4442	0.1837
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0031	1.1999	0.8334
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5060
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0055	0.2991	3.3428
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0706			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0140
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0667	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 114

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 115

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0026	7.6272	0.1311
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0120	0.0052	2.3025	0.4343
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0051	0.1440	6.9448
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0042	0.0137	0.3084	3.2426
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0066	0.0276	0.2393	4.1785
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

FETUS
% frequency

Development	0.0139
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0000
Lung	0.0020
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0083
Uterus_n	

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Electronic Northern for SEQ. ID NO.: 116

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0624	0.0204	3.0509	0.3278
Breast	0.0102	0.0000	undef	0.0000
Small intestine	0.0368	0.0165	2.2244	0.4496
Ovary	0.0120	0.0026	4.6050	0.2172
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0556	0.0000	undef	0.0000
Brain	0.0030	0.0041	0.7200	1.3890
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0190	0.0065	2.9412	0.3400
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0290	0.0230	1.2605	0.7933
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0110	0.2991	3.3428
Penis	0.1258	0.0000	undef	0.0000
Prostate	0.0479	0.0319	1.5013	0.6661
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.0272	3.9279	0.2546
Uterus-general	0.0509	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0167	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0060
Prostate	0.0499	Prostate	0.0342
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0541

Electronic Northern for SEQ. ID NO.: 117

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0068	0.0150	0.4528	2.2083
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0051	0.1440	6.9448
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0064	0.0137	0.4626	2.1618
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0063	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0089	0.0000	undef	0.0000
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0026	0.0000	undef
White blood cells	0.0026	0.0000	undef	0.0000
Cervix	0.0000	0.0000	undef	undef

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000	Breast 0.0000
Gastrointestinal	0.0000	Ovary_n 0.1595
Brain	0.0000	Ovary_t 0.0000
Hematopoietic	0.0000	Endocrine tissue 0.0000
Skin	0.0000	Fetal 0.0006
Hepatic	0.0000	Gastrointestinal 0.0000
Heart-blood vessels	0.0000	Hematopoietic 0.0114
Lung	0.0000	Skin-muscle 0.0065
Suprarenal gland	0.0000	Testicles 0.0154
Kidney	0.0000	Lung 0.0000
Placenta	0.0061	Nerves 0.0020
Prostate	0.0000	Prostate 0.0068
Sensory organs	0.0000	Sensory Organs 0.0077
		Uterus n 0.0000

Electronic Northern for SEQ. ID NO.: 119

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0819	0.0383	2.1356	0.4682
Breast	0.0473	0.0320	1.4811	0.6752
Small intestine	0.0460	0.0331	1.3903	0.7193
Ovary	0.0539	0.0442	1.2190	0.8204
Endocrine tissue	0.0494	0.0652	0.7576	1.3199
Gastrointestinal	0.0805	0.0139	5.7984	0.1725
Brain	0.0451	0.0390	1.1557	0.8653
Hematopoietic	0.0374	0.0379	0.9881	1.0121
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0190	0.0323	0.5882	1.7000
Heart	0.0382	0.0825	0.4626	2.1618
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0384	0.0184	2.0886	0.4788
Stomach-esophagus	0.0580	0.0537	1.0805	0.9255
Muscle-skeleton	0.0514	0.0240	2.1416	0.4669
Kidney	0.0489	0.0479	1.0196	0.9808
Pancreas	0.0330	0.0663	0.4986	2.0057
Penis	0.0359	0.0000	undef	0.0000
Prostate	0.0610	0.0617	0.9883	1.0118
Uterus-endometrium	0.2838	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0509	0.0000	undef	0.0000
Breast hyperplasia	0.2206			
Prostate hyperplasia	0.0773			
Seminal vesicle	0.0089			
Sensory organs	0.0353			
White blood cells	0.0737			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0278	Breast	0.0340
Gastrointestinal	0.0361	Ovary_n	0.1595
Brain	0.0125	Ovary_t	0.0101
Hematopoietic	0.0157	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0233
Hepatic	0.0260	Gastrointestinal	0.0488
Heart-blood vessels	0.0818	Hematopoietic	0.0285
Lung	0.0325	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0432	Lung	0.0164
Placenta	0.0303	Nerves	0.0261
Prostate	0.0000	Prostate	0.1163
Sensory organs	0.0126	Sensory Organs	0.0929
		Uterus_n	0.0416

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0195	0.0000	undef	0.0000	
Breast	0.0026	0.0038	0.6805	1.4694	
Small intestine	0.0031	0.0000	undef	0.0000	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0017	0.0025	0.6792	1.4722	
Gastrointestinal	0.0038	0.0000	undef	0.0000	
Brain	0.0052	0.0041	1.2599	0.7937	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0011	0.0000	undef	0.0000	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0020	0.0000	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0034	0.0000	undef	0.0000	
Kidney	0.0027	0.0000	undef	0.0000	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0022	0.0000	undef	0.0000	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0026				
White blood cells	0.0106				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0070
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 121

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0273	0.0051	5.3391	0.1873
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0059	0.0041	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 122

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0351	0.0077	4.5763	0.2185
Breast	0.0077	0.0038	2.0416	0.4898
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0115	0.0093	1.2425	0.8048
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0233	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0599	0.0000	undef	0.0000
Prostate	0.0131	0.0149	0.8774	1.1397
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0340	0.4489	2.2276
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0278	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0391	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 123

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0390	0.0051	7.6272	0.1311
Breast	0.0064	0.0056	1.1342	0.8817
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0154	0.0060	2.5700	0.3891
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0272	0.5611	1.7821
Uterus-general	0.0128	0.0000	undef	undef
Breast hyperplasia	0.0039			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 124

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0026	7.6272	0.1311
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0109	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0087	0.0043	2.0473	0.4885
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0260	Gastrointestinal	0.0006
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0162
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0390	0.0051	7.6272	0.1311
Breast	0.0153	0.0150	1.0208	0.9796
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0210	0.0078	2.6863	0.3723
Endocrine tissue	0.0170	0.0125	1.3585	0.7361
Gastrointestinal	0.0153	0.0000	undef	0.0000
Brain	0.0126	0.0133	0.9415	1.0622
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0114	0.0143	0.7983	1.2526
Stomach-esophagus	0.0097	0.0307	0.3151	3.1733
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0326	0.0274	1.1896	0.8406
Pancreas	0.0033	0.0166	0.1994	5.0142
Penis	0.0629	0.0000	undef	0.0000
Prostate	0.0109	0.0170	0.6398	1.5631
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0068	4.4891	0.2228
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0191			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0051
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0076
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0057
Suprarenal gland	0.0254	Testicles	0.0162
Kidney	0.0062	Lung	0.0077
Placenta	0.0000	Nerves	0.0082
Prostate	0.0000	Prostate	0.0120
Sensory organs	0.0126	Sensory Organs	0.0205
		Uterus_n	0.0000
			0.0749

Electronic Northern for SEQ. ID NO.: 126

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0085	0.0075	1.1321	0.8833
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0059	0.0134	0.3840	2.6043
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0201	0.0137	1.4649	0.6827
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0145	0.0164	0.8891	1.1248
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0017	0.0300	0.0571	17.5100
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0204	2.2445	0.4455
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0470			
White blood cells	0.0121			
Cervix	0.0213			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0217
Suprarenal gland	0.0254
Kidney	0.0185
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0210
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory Organs	0.0387
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 127

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0090	0.0019	4.7637	0.2099
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0240	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0312	0.0000	undef 0.0000
Breast	0.0079	0.0056	1.4090 0.7097
Large intestine	0.0077	0.0000	undef 0.0000
Small intestine	0.0027	0.0107	0.2577 3.8812
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0048	0.0089	0.5432 1.8409
Brain	0.0029	0.0080	0.3627 2.7574
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0020	0.0000	undef 0.0000
Testicles	0.0000	0.0118	0.0000 undef
Lung	0.0010	0.0037	0.2631 3.8007
Stomach-esophagus	0.0217	0.0000	undef 0.0000
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9285 1.0770
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0066	0.0039	1.6882 0.5923
T lymphoma	0.0025	0.0149	0.1691 5.9152
Uterus	0.0030	0.0046	0.6426 1.5563
White blood cells	0.0021	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

	FETUS % freq.
Development	0.0278
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0126
Sensory organs	

Breast	
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0245
Gastrointestinal	0.0064
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0065
Testicles_t	0.0167
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0060
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0182
White blood cells	0.0000

Electronic Northern for Seq. ID: 392

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0059	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerve_s	0.0010
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

"0000" 04924953

Electronic Northern for Seq. ID: 393

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder	0.0075	0.0000	undef	0.0000
Breast	0.0195	0.0000	undef	0.0000
Large intestine	0.0009	0.0000	undef	0.0000
Small intestine	0.0057	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0046	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0055	0.0000	undef
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary-t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles n	0.0042
Testicles-t	0.0000
Lungs n	0.0000
Lungs-t	0.0000
Nerve	0.0020
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

"00000" 04922959

Electronic Northern for Seq. ID: 394

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0156	0.0023	6.6380 0.1506
Breast	0.0035	0.0042	0.8349 1.1977
Large intestine	0.0038	0.0199	0.1922 5.2023
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0059	0.0024	2.4887 0.4018
Endocrine tissue	0.0080	0.0000	undef 0.0000
Brain	0.0023	0.0040	0.5803 1.7234
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0030	0.0000	undef 0.0000
Testicles	0.0000	0.0059	0.0000 undef
Lung	0.0019	0.0053	0.3508 2.8506
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9285 1.0770
Pancreas	0.0033	0.0110	0.2992 3.3427
Prostate	0.0057	0.0026	2.1706 0.4607
T lymphoma	0.0051	0.0149	0.3381 2.9576
Uterus	0.0015	0.0000	undef 0.0000
White blood cells	0.0021	0.0304	0.0676 14.7861
Hematopoietic	0.0013		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	
Breast t	0.0136
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0051
Fetal	0.0000
Gastrointestinal	0.0017
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0293
Nerves	0.0000
Kidney t	0.0040
Ovary uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0000
White blood cells	0.0000
	0.0000

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Electronic Northern for Seq. ID: 395

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0156	0.0047	3.3192	0.3013
Breast	0.0062	0.0183	0.3372	2.9657
Large intestine	0.0019	0.0114	0.1682	5.9454
Small intestine	0.0000	0.0107	0.0000	undef
Ovary	0.0030	0.0072	0.4148	2.4110
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0006	0.0010	0.6045	1.6542
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0190	0.0000	undef
Heart	0.0020	0.0962	0.0211	47.4018
Testicles	0.0000	0.0000	undef	undef
Lung	0.0039	0.0111	0.3508	2.8506
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0171	0.0037	4.6389	0.2156
Kidney	0.0045	0.0000	undef	0.0000
Pancreas	0.0000	0.0110	0.0000	undef
Prostate	0.0000	0.0052	0.0000	undef
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0278
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0071
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary_uterus	0.0113
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

"00000" 0.0000000000

Electronic Northern for Seq. ID: 396

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0000	0.0136	0.0000 undef
Breast	0.0429	0.0000	undef 0.0000
Large intestine	0.0000	0.0042	0.0000 undef
Small intestine	0.0038	0.0000	undef 0.0000
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0032	0.0000	undef 0.0000
Skin	0.0012	0.0010	1.1605 0.8617
Hepatic	0.0037	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0055	0.0000 undef
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0017	0.0037	0.4639 2.1557
Pancreas	0.0045	0.0000	undef 0.0000
Prostate	0.0017	0.0000	undef 0.0000
T lymphoma	0.0009	0.0026	0.3618 2.7643
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0030	0.0000	undef 0.0000
Hematopoietic	0.0007	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0054		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0249
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0075
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0084
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney t	0.0070
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0077
	0.0000

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Electronic Northern for Seq. ID: 397

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0117	0.0000	undef	0.0000
Breast	0.0009	0.0000	undef	0.0000
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0048	0.0000	undef	0.0000
Brain	0.0006	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0019	0.0018	1.0524	0.9502
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0009	0.0026	0.3618	2.7643
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0051
Fetal	0.0000
Gastrointestinal	0.0070
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0293
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0135
Sensory organs	0.0061
White blood cells	0.0000

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Electronic Northern for Seq. ID: 398

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0156	0.0023	6.6384 0.1506
Breast	0.0053	0.0042	1.2524 0.7985
Large intestine	0.0000	0.0028	0.0000 undef
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0024	1.2443 0.8037
Endocrine tissue	0.0000	0.0057	0.0000 undef
Brain	0.0024	0.0060	0.4030 2.4814
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0030	0.0137	0.2215 4.5145
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0068	0.0037	1.8417 0.5430
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0000	0.0055	0.0000 undef
Prostate	0.0028	0.0026	1.0853 0.9214
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0000	0.0092	0.0000 undef
White blood cells	0.0082	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0054		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 399

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0234	0.0047	4.9788 0.2009
Breast	0.0070	0.0098	0.7157 1.3973
Large intestine	0.0057	0.0085	0.6728 1.4864
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0059	0.0000	undef 0.0000
Endocrine tissue	0.0032	0.0038	0.8479 1.1794
Brain	0.0018	0.0020	0.9068 1.1028
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0046	0.0190	0.2441 4.0960
Heart	0.0081	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0068	0.0018	3.6834 0.2715
Stomach-esophagus	0.0072	0.0064	1.1333 0.8824
Muscle-skeleton	0.0069	0.0000	undef 0.0000
Kidney	0.0067	0.0096	0.6963 1.4362
Pancreas	0.0033	0.0221	0.1496 6.6857
Prostate	0.0094	0.0052	1.8088 0.5529
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0093	0.0000	undef 0.0000
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.1595
Endocrine tissue	0.0101
Fetal	0.0000
Gastrointestinal	0.0046
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles_n	0.0130
Testicles_t	0.0125
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0000
White blood cells	0.0000

T09929 "T09929" T09929

Electronic Northern for Seq. ID: 400		RATIOS	
	NORMAL % freq.	TUMOR % freq.	N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0156	0.0000	undef 0.0000
Breast	0.0018	0.0000	undef 0.0000
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0016	0.0019	0.8479 1.1794
Skin	0.0018	0.0010	1.8135 0.5514
Hepatic	0.0073	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0020	0.0000	undef 0.0000
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0033	0.0000	undef 0.0000
T lymphoma	0.0047	0.0026	1.8088 0.5529
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0031	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000		
Seminal vesicle	0.0027		
Sensory organs	0.0000		

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0110
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0040
Ovary_uterus	0.0000
Ovary_uterus	0.0045
Prostate_n	0.0000
Prostate_n	0.0121
Sensory_organ	0.0000
Sensory_organ	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 401

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0125	0.0136	0.9198 1.0872
Bladder	0.0390	0.0094	4.1487 0.2410
Breast	0.0158	0.0056	2.8179 0.3549
Large intestine	0.0172	0.0028	6.0551 0.1652
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0178	0.0119	1.4932 0.6697
Endocrine tissue	0.0161	0.0195	0.8231 1.2150
Brain	0.0179	0.0170	1.0581 0.9451
Skin	0.0220	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0162	0.0275	0.5907 1.6929
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0175	0.0092	1.8944 0.5279
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0257	0.0037	6.9583 0.1437
Kidney	0.0201	0.0096	2.0891 0.4787
Pancreas	0.0066	0.0276	0.2393 4.1784
Prostate	0.0104	0.0000	undef 0.0000
T lymphoma	0.0051	0.0448	0.1127 8.8727
Uterus	0.0177	0.0276	0.6426 1.5563
White blood cells	0.0116	0.0407	0.1916 5.2186
Hematopoietic	0.0040		
Penis	0.0241		
Seminal vesicle	0.0070		
Sensory organs	0.0353		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0185
Placenta	0.1212
Prostate	0.0000
Sensory organs	0.0377

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0226
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0324
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0191
Kidney t	0.0000
Ovary uterus	0.0248
Prostate n	0.0061
Sensory organs	0.0077
White blood cells	0.0000

Electronic Northern for Seq. ID: 402

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0125	0.0000	undef 0.0000
Bladder	0.0429	0.0141	3.0424 0.3287
Breast	0.0387	0.0084	4.5922 0.2178
Large intestine	0.0038	0.0028	1.3456 0.7432
Small intestine	0.0165	0.0107	1.5459 0.6469
Ovary	0.0237	0.0000	undef 0.0000
Endocrine tissue	0.0177	0.0018	9.9589 0.1004
Brain	0.0041	0.0100	0.4062 2.4620
Skin	0.0514	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0457	0.0137	3.3227 0.3010
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0467	0.0296	1.5786 0.6335
Stomach-esophagus	0.0145	0.0064	2.2671 0.4411
Muscle-skeleton	0.0171	0.0222	0.7731 1.2934
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0075	0.0052	1.4470 0.6911
T lymphoma	0.0051	0.0000	undef 0.0000
Uterus	0.0281	0.0138	2.0348 0.4915
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0160		
Penis	0.0295		
Seminal vesicle	0.0141		
Sensory organs	0.0353		

FETUS
% freq.

Development	0.0418
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0325
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0476
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0220
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0583
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0090
Kidney_t	0.0000
Ovary uterus	0.0405
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

T09000 04954959

Electronic Northern for Seq. ID: 403

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0351	0.0047	7.4677	0.1339
Breast	0.0070	0.0014	5.0097	0.1996
Large intestine	0.0115	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0016	0.0035	0.4527	2.2091
Brain	0.0017	0.0060	0.2901	3.4467
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0020	0.0137	0.1477	6.7715
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0039	0.0018	2.1049	0.4751
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0112	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2992	3.3427
Prostate	0.0075	0.0026	2.8941	0.3455
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0059	0.0046	1.2851	0.7781
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0254
Adrenal gland	0.0185
Kidney	0.0121
Placenta	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

Consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will accordingly

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from normal bladder tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4

Mapping of Nucleic Acid Sequences on the Human Genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq. ID No.	Identified BACs		
60	311/K/13	271/E/3	252/P/20
102	458/N/24	349/F/12	

TABLE I

Col. 1 - Sequence ID

Col. 2 - Expression

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Cytogenetic localization

Col. 6 - Nearest marker

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TABLE I

Sequence ID	Expression	Function
1	Overexpressed in normal bladder tissue	H. sapiens rap1b
2	Overexpressed in normal bladder tissue	Human zinc finger transcription factor hEZF (EZF) homolog
3	Overexpressed in normal bladder tissue	Homo sapiens mRNA for phosphatidic acid phosphatase 2a
4	Overexpressed in normal bladder tissue	H. sapiens mRNA for G protein-coupled receptor Edg-2
6	Overexpressed in normal bladder tissue	Homo sapiens secreted frizzled-related protein
7	Overexpressed in normal bladder tissue	Human monocytic leukemia zinc finger protein (MOZ)
8	Overexpressed in normal bladder tissue	Homo sapiens angiotensin II receptor
9	Overexpressed in normal bladder tissue	Human mRNA for RNA helicase (HRH1)
12	Overexpressed in normal bladder tissue	H. sapiens rhoB
13	Overexpressed in normal bladder tissue	Human skeletal muscle LIM-protein SLIM 1
14	Overexpressed in normal bladder tissue	Homo sapiens 39 kDa protein
17	Overexpressed in normal bladder tissue	H. sapiens dermatopontin mRNA
18	Overexpressed in normal bladder tissue	Homo sapiens phosphoglucomutase-related protein (PGMRP)

20	Overexpressed in normal bladder tissue	Human nucleic acid binding protein CNBP
21	Overexpressed in normal bladder tissue	Unknown
22	Overexpressed in normal bladder tissue	Human small nuclear ribonucleoprotein (U1-70K)
23	Overexpressed in normal bladder tissue	H. sapiens mRNA for telokin homolog
24	Overexpressed in normal bladder tissue	Homologous to pil2 from rats
25	Overexpressed in normal bladder tissue	Unknown
26	Overexpressed in normal bladder tissue	Unknown
27	Overexpressed in normal bladder tissue	Unknown
29	Overexpressed in normal bladder tissue	Homologous to sushi repeat protein
30	Overexpressed in normal bladder tissue	Unknown
31	Overexpressed in normal bladder tissue	Unknown
32	Overexpressed in normal bladder tissue	Unknown
33	Overexpressed in normal bladder tissue	Unknown
34	Overexpressed in normal bladder tissue	Unknown

35	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid F09E5
36	Overexpressed in normal bladder tissue	Unknown
37	Overexpressed in normal bladder tissue	Homologous to murine RING zinc finger protein
38	Overexpressed in normal bladder tissue	Rattus norvegicus cytoplasmic dynein intermediate chain 2c
39	Overexpressed in normal bladder tissue	Unknown
40	Overexpressed in normal bladder tissue	Unknown
43	Overexpressed in normal bladder tissue	Gry-rbp
44	Overexpressed in normal bladder tissue	Unknown
46	Overexpressed in normal bladder tissue	Unknown
47	Overexpressed in normal bladder tissue	Unknown
48	Overexpressed in normal bladder tissue	Unknown
50	Overexpressed in normal bladder tissue	Homologous to HU-K5
51	Overexpressed in normal bladder tissue	Unknown
52	Overexpressed in normal bladder tissue	Homologous to O. aries putative G- protein linked receptor (edg-2)

53	Overexpressed in normal bladder tissue	Unknown
54	Overexpressed in normal bladder tissue	Human homolog to murine NST-1
55	Overexpressed in normal bladder tissue	Homologous to human CIP4
56	Overexpressed in normal bladder tissue	Human Cbf5p homolog
57	Overexpressed in normal bladder tissue	Unknown
58	Overexpressed in normal bladder tissue	Unknown
59	Overexpressed in normal bladder tissue	Unknown
60	Overexpressed in normal bladder tissue	Unknown
61	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid TC9A5
62	Overexpressed in normal bladder tissue	Unknown
63	Overexpressed in normal bladder tissue	Unknown
65	Overexpressed in normal bladder tissue	Homologous to human KOX15
67	Overexpressed in normal bladder tissue	Unknown
69	Overexpressed in normal bladder tissue	Homologous to Golgi 4-transmembrane spanning transporter MTP

72	Overexpressed in normal bladder tissue	Unknown
73	Overexpressed in normal bladder tissue	Unknown
75	Overexpressed in normal bladder tissue	Human homolog to rat mRNA for V-1 protein
77	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid F 13G3
78	Overexpressed in normal bladder tissue	Unknown
79	Overexpressed in normal bladder tissue	Unknown
80	Overexpressed in normal bladder tissue	Human pyruvate dehydrogenase kinase isoform 4
82	Overexpressed in normal bladder tissue	Unknown
83	Overexpressed in normal bladder tissue	Unknown
85	Overexpressed in normal bladder tissue	Unknown
86	Overexpressed in normal bladder tissue	Mouse epithelial zinc-finger protein EZF (Zie)
88	Overexpressed in normal bladder tissue	Unknown
90	Overexpressed in normal bladder tissue	Unknown
92	Overexpressed in normal bladder tissue	Homologous to MyD118

93	Overexpressed in normal bladder tissue	Homologous to p8 protein from rats
94	Overexpressed in normal bladder tissue	Unknown
95	Overexpressed in normal bladder tissue	Unknown
96	Overexpressed in normal bladder tissue	Homologous to murine B-1ND1
97	Overexpressed in normal bladder tissue	Canis familiaris Sec61-complex gamma-subunit
98	Overexpressed in normal bladder tissue	Unknown
99	Overexpressed in normal bladder tissue	Human homolog to X taavis 146 kDa nuclear protein
100	Overexpressed in normal bladder tissue	Unknown
101	Overexpressed in normal bladder tissue	Human dysferlin
102	Overexpressed in normal bladder tissue	Unknown
103	Overexpressed in normal bladder tissue	Unknown
104	Overexpressed in normal bladder tissue	Unknown
105	Overexpressed in normal bladder tissue	Unknown
106	Overexpressed in normal bladder tissue	Unknown

107	Overexpressed in normal bladder tissue	Unknown
108	Overexpressed in normal bladder tissue	Homologous to APRIL
109	Overexpressed in normal bladder tissue	Homologous to the human p20
110	Overexpressed in normal bladder tissue	Unknown
111	Overexpressed in normal bladder tissue	Unknown
112	Overexpressed in normal bladder tissue	Unknown
113	Overexpressed in normal bladder tissue	Homologous to D. melanogaster furrowed
114	Overexpressed in normal bladder tissue	Homologous to murine BRX protein
115	Overexpressed in normal bladder tissue	Unknown
116	Overexpressed in normal bladder tissue	Unknown
117	Overexpressed in normal bladder tissue	Caenorhabditis elegans cosmid R08D7
118	Overexpressed in normal bladder tissue	Unknown
119	Overexpressed in normal bladder tissue	HSP 86
120	Overexpressed in normal bladder tissue	Homologous to human AKAP95

121	Overexpressed in normal bladder tissue	Sus scrofa mRNA for 17-kDa PKC- potentiated inhibitory protein of PP1
122	Overexpressed in normal bladder tissue	Unknown
123	Overexpressed in normal bladder tissue	Homo sapiens supervillin
124	Overexpressed in normal bladder tissue	Homologous to B. taurus vacuolar ATPase subunit A
125	Overexpressed in normal bladder tissue	SH3 domain binding glutamic acid- rich-like protein
126	Overexpressed in normal bladder tissue	Human homolog to Mus musculus WSB-1
127	Overexpressed in normal bladder tissue	Unknown
391	Lengthening to Seq. ID No: 27	
392	Lengthening to Seq. ID No: 34	
393	Lengthening to Seq. ID No: 50	
394	Lengthening to Seq. ID No: 56	
395	Lengthening to Seq. ID No: 78	
396	Lengthening to Seq. ID No: 82	
397	Lengthening to Seq. ID No: 88	
398	Lengthening to Seq. ID No: 100	
399	Lengthening to Seq. ID No: 101	

400	Lengthening to Seq. ID No: 102	
401	Lengthening to Seq. ID No: 104	
402	Lengthening to Seq. ID No: 110	
403	Lengthening to Seq. ID No: 111	

[Key to Table I:]

[Column 4: Sequence ID No. 109:] crystallin = crystalline

[Column 6: Sequence ID Nos. 6, 7, 9, 22, 29, 31-34, 39, 43, 46,
48, 50, 51, 56, 58-62, 65, 72, 73, 82, 86, 102,
103, 111, 112, 115, 126:] ... bis ... = ... to ...

"BIBL" 04924950

TABELLE I

Sequenz ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
1	in Blasennormalgewebe überexprimiert	H.sapiens rap1b	ras	6q21-q22.1	D6S304-D6S1639
2	in Blasennormalgewebe überexprimiert	Human zinc finger transcription factor hEZF (EZF) Homolog	ZINC_FINGER_C2H2_2		
3	in Blasennormalgewebe überexprimiert	Homo sapiens mRNA for phosphatidic acid phosphatase 2a			
4	in Blasennormalgewebe überexprimiert	H.sapiens mRNA for G protein-coupled receptor Edg-2	7tm_1	9q31.3-q32	D9S1690-D9S279
6	in Blasennormalgewebe überexprimiert	Homo sapiens secreted frizzled-related protein	FZ DOMAIN; NETRIN_CT; PRO_RICH	8p11.23-p12	SHGC-5722 bis SHGC-5765
7	in Blasennormalgewebe überexprimiert	Human monocytic leukaemia zinc finger protein (MOZ)		8p11.23-p12	D8S2070 bis SHGC-31558
8	in Blasennormalgewebe überexprimiert	Homo Sapiens angiotensin II receptor		22q11.22-q11.23	D6S2136-D4S3274
9	in Blasennormalgewebe überexprimiert	Human mRNA for RNA helicase (HRH1)		6p21.31	SHGC-17229 bis D6S478
12	in Blasennormalgewebe überexprimiert	H.sapiens rhoB		2p23.3	D2S387
13	in Blasennormalgewebe überexprimiert	Human skeletal muscle LIM-protein SLIM1	LIM_DOMAIN_2	Xq25-q27.2	DXS994-DXS1062
14	in Blasennormalgewebe überexprimiert	Homo sapiens 39 kDa protein	PDZ; LIM	4q34.1-q35.2	D4S408-D4S426
17	in Blasennormalgewebe überexprimiert	H.sapiens dermatopontin mRNA		1q23.1-q23.2	D1S445-D1S2750
18	in Blasennormalgewebe überexprimiert	Homo sapiens phosphoglucomutase-related protein (PGMRP)	PGM_PMM	9p11.1-q12	D9S1699
20	in Blasennormalgewebe überexprimiert	Human nucleic acid binding protein CNBP	zf-CCHC	3q13.31-q21.1	D3S1589-D3S1766
21	in Blasennormalgewebe überexprimiert	unbekannt			
22	in Blasennormalgewebe überexprimiert	Human small nuclear ribonucleoprotein (U1-70K)		19q13.31-q13.33	SHGC-36947 bis SHGC-34723
23	in Blasennormalgewebe überexprimiert	H.sapiens mRNA for telokin Homolog			
24	in Blasennormalgewebe überexprimiert	Homolog zu pil2 aus Ratte			

Sequenz ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
25	in Blasennormalgewebe überexprimiert	unbekannt			
26	in Blasennormalgewebe überexprimiert	unbekannt			
27	in Blasennormalgewebe überexprimiert	unbekannt		5q32-q33.1	D5S470
29	in Blasennormalgewebe überexprimiert	Homolog zu sushi repeat protein	PRO_RICH	3q11.2	SHGC-36351 bis SHGC-14633
30	in Blasennormalgewebe überexprimiert	unbekannt		2q37.3	D2S206-D2S331
31	in Blasennormalgewebe überexprimiert	unbekannt		2q31.1-q31.3	WI-7596 bis D2S326
32	in Blasennormalgewebe überexprimiert	unbekannt		20p13	D20S864 bis SHGC-34269
33	in Blasennormalgewebe überexprimiert	unbekannt		13q12.11-q12.3	SHGC-2665 bis D13S289
34	in Blasennormalgewebe überexprimiert	unbekannt		9q21.31	SHGC-32247 bis SHGC-5528
35	in Blasennormalgewebe überexprimiert	Caenorhabditis elegans cosmid F09E5	UPF0001		
36	in Blasennormalgewebe überexprimiert	unbekannt			
37	in Blasennormalgewebe überexprimiert	Homolog zu murinem RING zinc finger protein	PRO_RICH; ZF_RING	17p13.3	D17S1548
38	in Blasennormalgewebe überexprimiert	Rattus norvegicus cytoplasmic dynein intermediate chain 2c	WD40_REGION	10q11.21	D10S604-D10S220
39	in Blasennormalgewebe überexprimiert	unbekannt		13q33.3	SHGC-9496 bis D13S1223
40	in Blasennormalgewebe überexprimiert	unbekannt			
43	in Blasennormalgewebe überexprimiert	Gry-rbp	RBD	20p13	D20S816 bis SHGC-33687
44	in Blasennormalgewebe überexprimiert	unbekannt			
46	in Blasennormalgewebe überexprimiert	unbekannt		2q21.3-q22.1	SHGC-35092 bis SHGC-32856
47	in Blasennormalgewebe überexprimiert	unbekannt			

Sequenz ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
48	in Blasennormalgewebe überexprimiert	unbekannt		15q11.2-q15.3	SHGC-35142 bis SHGC-7407
50	in Blasennormalgewebe überexprimiert	Homolog zu HU-K5		3q21.3-3q23	SHGC-37132 bis SHGC-30693
51	in Blasennormalgewebe überexprimiert	unbekannt		3p21.31-p21.1	SHGC-30574 bis SHGC-31529
52	in Blasennormalgewebe überexprimiert	Homolog zu O. aries Putative G-protein linked receptor (edg-2)			
53	in Blasennormalgewebe überexprimiert	unbekannt			
54	in Blasennormalgewebe überexprimiert	Humanes Homolog zu murinem NST-1	HSP70		
55	in Blasennormalgewebe überexprimiert	Homolog zu humanem CIP4			
56	in Blasennormalgewebe überexprimiert	Humanes Cbf5p Homolog		Xq25-q27.3	SHGC-31168 bis AFM207xb8
57	in Blasennormalgewebe überexprimiert	unbekannt	ZF_DHHC; NLS_BP		
58	in Blasennormalgewebe überexprimiert	unbekannt		9q12	WI-7387 bis SHGC-32868
59	in Blasennormalgewebe überexprimiert	unbekannt		9q22.2-q22.31	SHGC-14680 bis SHGC-8725
60	in Blasennormalgewebe überexprimiert	unbekannt		1p36.13-p36.31	SHGC-34104 bis SHGC-9861
61	in Blasennormalgewebe überexprimiert	Caenorhabditis elegans cosmid T09A5		Chr.5	SHGC-2758 bis SHGC-4278
62	in Blasennormalgewebe überexprimiert	unbekannt		1q32.3	SHGC-15949 bis SHGC-11476
63	in Blasennormalgewebe überexprimiert	unbekannt	Oxysterol_BP	1p32.3-p33	D1S197-D1S417
65	in Blasennormalgewebe überexprimiert	Homolog zu humanem KOX15	ZINC_FINGER_C2H2_2	16q21-q23.1	D16S2624 bis SHGC-9008
67	in Blasennormalgewebe überexprimiert	unbekannt			
69	in Blasennormalgewebe überexprimiert	Homolog zu Golgi 4-Transmembran spanning Transporter MTP		8q22.3-q24.13	D8S556-D8S266
72	in Blasennormalgewebe überexprimiert	unbekannt		10q23.1	SHGC-14535 bis SHGC-30780

Sequenz ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
73	in Blasennormalgewebe überexprimiert	unbekannt		1q22	SHGC-32839 bis D1S1576
75	in Blasennormalgewebe überexprimiert	Humanes Homolog zu Rat mRNA for V-1 protein	ank		
77	in Blasennormalgewebe überexprimiert	Caenorhabditis elegans cosmid F13G3	Ribosomal_L13	8q23.3-q24.11	WI-5098-CHLC.GATA8G03.443
78	in Blasennormalgewebe überexprimiert	unbekannt	ig		
79	in Blasennormalgewebe überexprimiert	unbekannt			
80	in Blasennormalgewebe überexprimiert	Humane Pyruvate Dehydrogenase Kinase Isoform 4		7q21.2-q22.1	D7S492-D7S652
82	in Blasennormalgewebe überexprimiert	unbekannt		3p24.3-p23	SHGC-9648 bis SHGC-14769
83	in Blasennormalgewebe überexprimiert	unbekannt		3p12.1-p21.1	D3S3117
85	in Blasennormalgewebe überexprimiert	unbekannt			
86	in Blasennormalgewebe überexprimiert	Mouse epithelial zinc-finger protein EZF (Zie)		9q22.33-q31.1	D9S1690 bis SHGC-14345
88	in Blasennormalgewebe überexprimiert	unbekannt		1p35.1	D1S2569-D1S2676
90	in Blasennormalgewebe überexprimiert	unbekannt			
92	in Blasennormalgewebe überexprimiert	Homolog zu MyD118			
93	in Blasennormalgewebe überexprimiert	Homolog zum p8 Protein aus Ratte	ras	16p11.2-q12.1	D16S3093-D16S409
94	in Blasennormalgewebe überexprimiert	unbekannt		14q11.1-q11.2	D14S990-D14S264
95	in Blasennormalgewebe überexprimiert	unbekannt		16p13.2-p13.3	D16S521
96	in Blasennormalgewebe überexprimiert	Homolog zu murinem B-IND1		15q22.31-q22.33	D15S159-D15S125
97	in Blasennormalgewebe überexprimiert	Canis familiaris Sec61-complex gamma-subunit	SecE		
98	in Blasennormalgewebe überexprimiert	unbekannt		16p21.2-p21.31	D6S276-D6S439

Sequenz ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
99	in Blasennormalgewebe überexprimiert	Humanes Homolog zu X laevis 146 kDa nuclear protein		2q23.3-q33.3	D2S117-D2S115
100	in Blasennormalgewebe überexprimiert	unbekannt	NLS_BP	9q22.31-q31.1	D9S176-D9S277
101	in Blasennormalgewebe überexprimiert	Humanes Dysferlin	PRO_RICH; C2_DOMAIN_2		
102	in Blasennormalgewebe überexprimiert	unbekannt		10q25.3	D10S216 bis SHGC-13269
103	in Blasennormalgewebe überexprimiert	unbekannt		2p23.1-p23.2	D2S2573 bis SHGC-15275
104	in Blasennormalgewebe überexprimiert	unbekannt	PRO_RICH	8p11.23-p12	D8S2102
105	in Blasennormalgewebe überexprimiert	unbekannt		1p31.1-p34.1	SHGC-32050
106	in Blasennormalgewebe überexprimiert	unbekannt		13q21.33-q22.1	D13S156-D13S162
107	in Blasennormalgewebe überexprimiert	unbekannt			
108	in Blasennormalgewebe überexprimiert	Homolog zu APRIL	TNF		
109	in Blasennormalgewebe überexprimiert	Homolog zu dem humanem p20	crystallin; HSP20	19q13.13	D19S425-D19S224
110	in Blasennormalgewebe überexprimiert	unbekannt		7q31.31	D7S522-D7S2756
111	in Blasennormalgewebe überexprimiert	unbekannt		10q23.31-q24.1	WI-7908 bis SHGC-34547
112	in Blasennormalgewebe überexprimiert	unbekannt		1q31.1-q31.3	SHGC-34113 bis SHGC-34344
113	in Blasennormalgewebe überexprimiert	Homolog zu D. melanogaster furrowed	sushi	9q31.3-q32	D9S160-D9S279
114	in Blasennormalgewebe überexprimiert	Homolog zu murinem BRX Protein	PRO_RICH		
115	in Blasennormalgewebe überexprimiert	unbekannt		Chr.17 (17p13.3-q25.3)	SHGC-33067 bis SHGC-32338
116	in Blasennormalgewebe überexprimiert	unbekannt		4q28.1-q31.1	D4S1580-D4S427
117	in Blasennormalgewebe überexprimiert	Caenorhabditis elegans cosmid R08D7			

Sequenz ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nearest Marker
118	in Blasennormalgewebe überexprimiert	unbekannt	PRO_RICH		
119	in Blasennormalgewebe überexprimiert	HSP 86	HSP90	11q13.2-q13.5	D11S913-D11S1314
120	in Blasennormalgewebe überexprimiert	Homolog zu humanem AKAP95	PRO_RICH		
121	in Blasennormalgewebe überexprimiert	Sus scrofa mRNA for 17-kDa PKC-potentiated inhibitory protein of PP1	PRO_RICH	19q13.13-q13.2	D19S1069-D19S421
122	in Blasennormalgewebe überexprimiert	unbekannt		1q32.1	D1S306-D1S2570
123	in Blasennormalgewebe überexprimiert	Homo sapiens Supervillin	PRO_RICH		
124	in Blasennormalgewebe überexprimiert	Homolog zu B.taurus vacuolar ATPase subunit A		3q11.2-q21.1	D3S2353-D3S3526
125	in Blasennormalgewebe überexprimiert	SH3 domain binding glutamic acid-rich-like protein		domain	binding
126	in Blasennormalgewebe überexprimiert	Humanes Homolog zu Mus musculus WSB-1	WD40_REGION; WD40; SOCS_DOMAIN	17p11.2	D17S783 bis SHGC-30289
127	in Blasennormalgewebe überexprimiert	unbekannt			
391	Verlängerung zu Seq ID No: 27				
392	Verlängerung zu Seq ID No: 34				
393	Verlängerung zu Seq ID No: 50				
394	Verlängerung zu Seq ID No: 56				
395	Verlängerung zu Seq ID No: 78				
396	Verlängerung zu Seq ID No: 82				
397	Verlängerung zu Seq ID No: 88				
398	Verlängerung zu Seq ID No: 100				
399	Verlängerung zu Seq ID No: 101				

Sequenz ID	Expression	Funktion	Module	Cylogenetische Lokalisation	Nearest Marker
400	Verlängerung zu Seq ID No: 102				
401	Verlängerung zu Seq ID No: 104				
402	Verlängerung zu Seq ID No: 110				
403	Verlängerung zu Seq ID No: 111				

TABLE II

Seq. ID No. Peptide Sequences (ORF's) Seq. ID. No.

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
21		430
		431
24		128
		129
25		131
		132
		133
26		134
		135
		136
27		137
		138
		139
29		143
30		144
		145
		146
		147
		148
		149
31		150
		151
		152
		153
32		154
		155
		156
33		157
		158
34		159
		160
		161
35		162
		163
		164
36		165
		166
		167
37		168
38		169
39		170
		171
40		172
		173
		174
43		181
44		182
		183
		184

"0909" 0402/950

Seq. ID No. Peptide Sequences (ORF's) Seq. ID. No.

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
46		188
		189
		190
47		191
		192
		193
48		194
		195
		196
50		200
		201
		202
51		203
		204
		205
52		206
		207
		208
53		209
54		210
55		211
56		212
		213
		214
57		215
58		216
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59		219
60		220
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61		224
		225
62		226
		227
		228
63		229
65		233
67		237
		238
		239
69		243
		244
72		251
		252
		253
73		254
		255
		256
75		260
77		264

"09090" 040902550

Seq. ID No.

Peptide Sequences (ORF's) Seq. ID. No.

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
78		265
		266
79		267
80		268
		269
		270
82		274
		275
		276
83		277
		278
		279
85		283
		284
		285
86		286
		287
		288
88		292
		293
		294
90		298
		299
		300
92		304
93		305
		306
94		307
95		308
		309
		310
96		311
		312
97		313
		314
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98		316
		317
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99		319
100		320
		321
101		322
102		323
		324
		325
103		326
		327
		328
104		329
		330
		331
105		332
		333

T05020"04022959

Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
106	334
	335
	336
107	337
	338
	339
108	340
	341
	342
109	343
	344
	345
110	346
	347
111	348
	349
	350
112	351
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113	354
114	355
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115	358
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117	365
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118	368
	369
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119	371
	372
120	373
	374
121	375
122	376
	377
122	378
123	379
	380
	381
124	382
	383
	384
125	385
	386
	387

Seq. ID No. Peptide Sequences (ORF's) Seq. ID. No.

Seq. ID. No.	Peptid-Sequenzen (ORF's)	Seq. ID. No.
126		388
127		389
		390
391		404
		405
392		406
		407
393		408
		409
394		410
		411
395		412
		413
396		414
		415
397		416
		417
398		418
		419
399		420
		421
400		422
		423
401		424
		425
402		426
		427
403		428
		429

The inventive nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 128-390 and 404-431 are described in the following sequence protocol.

Sequence Protocol**(1) GENERAL INFORMATION:****(i) APPLICANT:**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Normal Bladder Tissue

(iii) Number of sequences: 365

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 1:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

cgttgaagta gatgcacaac agtgtatgct tgaaatcttg gatactgcag gaacggagca 60
atttacagca atgagggatt tatacatgaa aaatggacaa ggatttgcat tagttttattc 120
catcacagca cagtccacat ttaacgattt acaagacctg agagaacaga ttcttcgagt 180

taaagacact gatgatgttc caatgattct tgttggtaat aagtgtgact tggaagatga 240
aagagttgta gggaagggaac aaggtcaaaa tctagcaaga caatggaaca actgtgcatt 300
cttagaactct tctgcaaaat caaaaataaa tgtaaatgag atcttttatg acctagtgcg 360
gcaaattaac agaaaaactc cagtgcctgg gaaggctcgc aaaaagtcac catgtcagct 420
gctttaatar actaaatgca ttgtagctct gagccaggctc tgaagaactg ttgccaatt 480
caacagtgcc agcattccaa ctttgttaaa cctaccaaca tcttaaatgg actttcctgt 540
gggtggtaccc tttaagaggc ggatgaaagc tactatatca gtttgacat tctaataact 600
ttccagtatc acaagagaga tttttactta tataatagtc ctagagtttg cagctggtaa 660
aaccagaggc tacatccagt attactgcta agagacattc ttcattccacc aatgttgtac 720
atgtatgaaa atggtgtact gtatacttta acatgcccc aactttgtat tggagagtac 780
aataatgtaa atcctaaaag caccactatt ttagcataat aaaagaaagt ccaaagagct 840
cctatataga ctactccaga taacttcgct tctttgatac ttgtagctta ttgtaatttt 900
ttttaagaaa ttcaaggctc ttattattgt acaaaataag cgctttgatt aacacagcta 960
tatagttttt ttaattttta aaaaacctgt ggagacgggtg atcttgcctt taaaacatga1020
tagtcctttc agtataatgt cttagattaa agacgttgcc tttaatatct gttgggaagg1080
aaatgtccag acttttcaaa tctcttatta tatgtttcct ttttttggtt acatagggaal1140
caatgtttat agtcgtgtgt acagtggggg tctacaacaa gaagtgtata ttttcaaaca1200
attttttaat gatttaacaa tttttgtaaa tcattttcag gcttctgcag ctgtagattc1260
tcaactgtgaa tcccttgctt gctcatgcac aagtgtattt gcaataccaa atatacaggt1320
ttagtatttt tgccctgttag tgattgtttc acatgtgtaa cgttttggtt gagatgttaa1380
atggtggacg agtactgtgg atgtgaatgt gggaagtaat tttaatcata tgtaattggt1440
cacaaggcct aatttgcatg aactattgct gttttattta acaatgcctt gttgctttgt1500
atgcattaat gtttggaagt aaagattgtg tgtctatcca acagggagcc acagtattta1560
aattgaocaa cctaattgta caactacttt gaggtggcca ttgtaaaact aaaagcctta1620
attaaagtgg tgcaattttg tataaacttag catcagtagt tcaataaatt tggattgccal680
tgcaagggct tgcattataa aaaaaacaa aaaaaaaaaa aa 1722

```

(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

cggtctgagg aggggggtctt ttgtgcacc cacttgggag ctggaccccc tctcagcaat 60
ggccaccggc cggctgcaca cgacttcccc ctggggcggc actccccagc aggactaccc 120
cgaccctggg tcttgaggaa gtgtgagca gcagggaactg tcaccctgcc ctgccgcttc 180
ctcccggtt ccatcccccac ccggggccca attaccatc cttcctgcc gatcagatgc 240
agccgcaagt cccgcccgtc cattaccaag agctcatgcc acccggttcc tgcagccag 300
aggagcccaa gccaaagagg ggaagacgat cgtggccccg gaaaaggacc gccaccaca 360
cttgtgatta cgcgggctgc ggcaaacct acacaaagag ttcccatctc aaggcacacc 420

tgcaaccca cacaggtgag aaaccttacc actgtgactg ggacggctgt ggatggaaat 480
tcgcccgtc agatgaactg accaggcact accgtaaaca cacggggcac cgcccgttcc 540
agtgcacaaa atgcgaccga gcattttcca ggtcggacca cctcgcctta cacatgaaga 600
ggcattttta aatcccagac agtggatatg acccacactg ccagaagaga attcagtatt 660
ttttactttt cacactgtct tcccgatgag ggaaggagcc cagccagaaa gcactacaat 720
catggtcaag ttcccaactg agtcattctg tgagtggata atcaggaaaa atgaggaatc 780
caaaagacaa aaatcaaaga acagatgggg tctgtgactg gatcttctat cattccaatt 840
ctaaatccga cttgaatatt cctggactta caaaatgcc agggggtgac tggaaagtgt 900
ggatatcagg gtataaatta tatccgtgag ttgggggagg gaagaccaga attcccttga 960
attgtgtatt gatgcaatat aagcataaaa gatcaccttg tattctcttt accttctaaa1020
agccattatt atgatgttag aagaagagga agaaattcag gtacagaaaa ccatgttta1080
atagccta at gatggtgtt gtgagcttg tcctaaaggt cccaacaagg gagccaaagg1140
tttaactgc tggatccttg gcaaggggaa atctgtgttt ttttccg 1187

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1478 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

"0902" 0102-2553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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gcgaacccgc gcgtgccccg gtcctgcgct gccagcggg aggggctgga ccccggttc 60
ctcctccctg ccggtcccca tccttaaagc gagagtctgg acgccccgcc tgtgggagag 120
agcgccggga tccggacggg gagcaaccgg ggcaggccgt gccggctgag gaggtcctga 180
ggctacagag ctgcccgcgc tggcacacga gcgcctcggc actaaccgag tgttcgcggg 240
ggctgtgagg ggagggcccc gggcgccatt gctggcggtg ggagcgccgc ccggtctcag 300
cccgccctcg gctgctctcc tcctccggct gggagggggc gtagctcggg gccgtcgcca 360
gccccggccc gggctcgaga atcaagggcc tcggccggcc tcccgcagct cagtccatcg 420
cccttgccgg gcagcccggg cagagaccat gtttgacaag acgcggtgc cgtacgtggc 480
cctcgatgtg ctctgcgtgt tgctggctgg attgcctttt gcaattctta cttcaaggca 540
taccoccttc caacgaggag tattctgtaa tgatgagtc atcaagtacc cttacaaaga 600
agacaccata ccttatgctg tattaggtgg aataatcatt ccattcagta ttatcgttat 660
tattcttggg gaaacccctg ctgttactg taaccttttg cactcaaatt cttttatcag 720
gaataactac atagccacta ttacaaaagc cattggaacc tttttatttg gtgcagctgc 780
tagtcagtc ctgactgaca ttgccaagta ttcaataggc agactgcggc ctacttctt 840
ggatgtttgt gatccagatt ggtcaaaaat caactgcagc gatggttaca ttgaatacta 900
catatgtcga ggaatgcag aaagagttaa ggaaggcagg ttgtccttct attcaggcca 960
ctcttcgttt tccatgtact gcatgctgtt tgtggcactt tatottcaag ccaggatgaa1020
gggagactgg gcaagactct tacgccccac actgcaattt ggtcttgtrg ccgtatccat1080

ttatgtgggc ctttctcgag tttctgatta taaacaccac tggagcgatg tgttgactgg1140
actcattcag ggagctctgg ttgcaatatt agttgctgta tatgtatcgg atttcttcaal1200
agaaagaact tcttttaaag aaagaaaaga ggaggactct catacaactc tgcataaaac1260
accaacaact gggaatcact atccgagcaa tcaccagcct tgaaaggcag cagggtgccc1320
aggtgaagct ggcctgtttt ctaaaggaaa atgattgcca caaggcaaga gggatgcatt1380
tttcttcctg ggtgtacaag cccttttaaa gaccttctgc tggctgcgat gcctcttgga1440
atgcacagtt gtgtgtaaca gatttacctt aactcgtg 1478

```

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 411 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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gccacatttc cgggggttttg cgggccccgc gatgttttcc agagcttttc aagtgggaag 60
aggagagcga caacgtgaaa atgccccgtg ccggggcgtc caccggagtc ctgccagctg120
tccggcgctg gggtggaagt ctgatttatg aagctcccca tccacctatc tgagtacctg180
acttctcagg actgacacct acagcatcag gtacacagct tctcctagca tgacttcgat240
ctgatcagca aacaagaaaa ttgtctccc gtagtcttgg ggcgtgttca ccacctacaa300
ccacagagct gtcatggctg ccatctctac ttocatccct gtaattttcac agccccagtt360
cacagccatg aatgaaccac agtgcttcta caacgagtc attgccttct t 411
```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3181 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

cgggtggggt gggagcaggg ggggacagt ccccggaac cgggtgggtc acacacacgc 60
 actgcgcctg tcagtagtgg acattgtaat ccagtcggct tgttcttgca gcattcccgc 120
 tcccttccct ccatagccac gctccaaacc ccagggtagc catggccggg taaagcaagg 180
 gccatttaga ttaggaaggt ttttaagatc cgcaatgtgg agcagcagcc actgcacagg 240
 aggaggtgac aaaccatttc caacagcaac acagccacta aaacacaaaa agggggattg 300
 ggcggaaagt gagagccagc agcaaaaact acattttgca acttgttggt gtggatctat 360
 tggctgatct atgcctttca actagaaaat tctaattgatt ggcaagtcac gttgttttca 420
 ggtccagagt agtttcttcc tgtctgcttt aaatggaaac agactcatac cacacttaca 480
 attaaggtca agcccagaaa gtgataagtg caggaggaa aagtgcaggt ccattatgta 540
 atagtgcagc caaagggacc aggggagagg cattgccttc tctgcccaca gtct ccjr 600
 gtgattgtct ttgaatctga atcagccagt ctgagatgcc ccaaagtttc ggttcctatg 660
 agccgggggc atgatctgat cccaagaca tgtggagggg cagcctgtgc ctgcctttgt 720
 gtcagaaaaa ggaaccaca gtgagcctga gagagacggc gattttcggg ctgagaaggc 780
 agtagttttc aaaaacacata gtaaaaaa aaacaaatga aaaaaatttt agaacagtcc 840
 agcaaatgct tagtcagggt gaattgtgaa attgggtgaa gagcttagga ttctaatttc 900
 atgttttttc cttttcacat ttttaaaaga acaattgacaa acacccactt atttttoag 960
 gtttaaaac agtctacatt gagcatttga aaggcgtgct agaacaagggt ctctgatcc1020
 gtccgaggtc gcttcccaga ggagcagctc tcccaggca tttgccaagg gaggcggatt1080
 tccctggtag tgtagctgtg tggctttcct tctgaagag tccgtgggtg ccctagaacc1140
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 a 3181

(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1964 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

19950101 09:02:45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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accagcagca  gctgtatggc  cgtagcccat  cggcagttgc  catgcaggct  ggccctcgcg  180
cactggctgt  tcagcgtggc  atgaacatgg  gggttaatct  gatgcctact  cccgcctata  240
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tgtgttgctc  ccaactccat  tctcttttct  ctctgtcaac  cagtttgccc  attctcttcc  1920
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(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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ggacacccca ggtatgtgga cgagcagttc ctgtcacgcc ttttccctatt tgtggccctg 60
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gctctggact ggtgacgtgc caccccaact cctggtgttt ggcttccctgg ctaatcttga 180
ctcctggaat cagtgggata agtaacacat caaggagtct tgtttcttca tcagagcttt 240
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cagttctgca ggtcctgact ctgcagaggg aagaggcaga aagagagaaa ctgtcagagt 420
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1702

"1999" 09/24/99

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2067 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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tctttgagga gggttataca aacaagggt tgaagattgc ctgcacccaa ccccgagag 180
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2067

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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cccgcgttac gcacaaagcc gccgatcccc ggctgggggt gagcagagcg accaccgccc 180
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(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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accaatgcac atgtagtaat caaatgtttg gggctagata ttatggtata caaaaaacat 60
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agtgatcata ttagcattta gcaaaaagca accctgcagc aaagtgaatt tctgtccggc1380
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aaaagtgcta atcatttagc cacttagtga tgtaagcaag aagcatagga gataaaaccc1500
ccactgagat gcctctcatg cctcagctgg gacccaccgt gtagacacac gacatgcaag1560
agttgcagcg gctgctccaa ctcactgctt caccocgttt ctgtggagcc gggagaaggg1620
accctactgg accatggcat ggggttaact ttcctcatca ggactctggc cct 1673

```

"BIBL" 0197255

(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

ggggccagga cgccgcccgg cgcggagtgg ctgccctgcg cggggacact cagagcccgg 60
tgggcgggag gaaggcggca tgcccagac ggtgatcctc ccgggcccctg cgccctgggg 120
cttcaggctc tcagggggca tagacttcaa ccagcctttg gtcataacca ggattacacc 180
aggaagcaag gcggcactgc caacctgtgt cctggagatg tcatcctggc tattgacggc 240
tttgggacag agtccatgac tcatgctgat ggcaggaca ggattaaagc agcagctcac 300
cagctgtgtc tcaaaattga caggggagaa actcacttat ggtctccaca agtatctgaa 360
gatgggaaag cccatccttt caaaatcaac ttagaatcag aaccacagga attcaaacc 420
attggtaccg cgcacaacag aaggggcccag ccttttggtg cagctgcaaa cattgatgac 480
aaaagacagg tagtgagcgc ttctataac tcgccaatg ggctctattc aactagcaat 540
atacaagatg cgcttcacgg acagctgcgg ggtctcattc ctagctcacc tcaaaacgag 600
cccacagcct cggtgcccc cagctcggag gtgtaccgga tgctccacga caatcggaat 660
gagccacac agcctcgcca gtcgggctcc ttcagagtgc tccaggggat ggtggacgat 720
ggctctgatg accgtccggc tggaaacggc agtgtgagag ctccggtgac gaaagtccat 780
ggcgggttcag gcggggcaca gaggatgccg ctctgtgaca aatgtgggag tggcatagtt 840
ggtgctgtgg tgaaggcggc ggataagtac cggcacccctg agtgcttcgt gtgtgccgac 900
tgcaacctca acctcaagca aaagggtac ttcttcatag aaggggagct gtactgcgaa 960
acccacgcaa gagcccgcac aaagcccca gagggctatg acacggtcac tctgtatccc1020
aaagcttaag tctctgcagg cgtggcacgc acgcacgcac ccacccacgc gcaattacac1080
gagaagacat tcatggcttt gggcagaagg attgtgcaga ttgtcaactc caaatctaaa1140
gtcaaggctc tagaccttta tctattggtt tattgaggaa aaggaatggg aggcaaatgc1200

ctgctatgtg aaaaaaacat acacttagct atgttttgca actctttttg gggctagcaal260
taatgatatt taaagcaata attttttgta tgtcatactc cacaatttac atgtatatta1320
cagccatcaa acacataaac atcaagatat ttgaaggact ctaattgtct ttcttgaca1380
agttgatttt gcaattgtgg taaatagcaa ataacaatct tgtattctaa cataatctgc1440
agttgtctgt atgtgtttta actattacag tgcattgttg ggagaaatc cctgaatttc1500
tttagttttg tattcaaaca attatgccac tcgatgcaac aaacataata aatacataaa1560
agatttaaaa aataaaaaaa aaaaaaaaaa aaa
1593

```

(2) INFORMATION ON SEQ ID NO. 17:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

cattgtttgc caaaatccca ggcagcatgg acctcagtct tctctgggta cttctgcccc 60
tagtcacccat ggccctggggc cagtattggcg attatggata cccataccag cagtatcatg 120
actacagcga tgatgggtgg gtgaatttga accggcaagg cttcagctac cagtgtcccc 180
aggggcaggt gatagtggcc gtgaggagca tcttcagcaa gaaggagggt tctgacagac 240
aatggaacta cgcctgcatg cccacaccac agagcctcgg ggaaccacag gagtgctggg 300
gggaggagat caacagggct ggcattggaat ggtaccagac gtgctccaac aatgggctgg 360
tggcaggatt ccagagccgc tacttcgagt cagtgtcggg tggggagtgg cagttttact 420
gttgctcgta cagcaagagg tgcccatatt cctgctgggt aacaacagaa tatccagggtc 480
actatgggtg ggaaatggac atgatttcct acaattatga ttactatatc cgaggagcaa 540
caaccacttt ctctgcagtg gaaagggatc gccagtggaa gttcataatg tgccggatga 600
ctgaatacga ctgtgaattt gcaaattgtt agatttgcca cataccaaat ctgggtgaaa 660
ggaaaggggc cggggacagg aggggtgtcca catatgttaa catcagttgg atctcctata 720
gaagtttctg ctgctctctt tcttctctcc tgagctggta actgcaatgc caacttcctg 780
ggcctttctg actagtatca cacttctaataaaaatccaca attaaaccat gtttctcact 840
tttcacatgt ttcatagcaa ctgctttata tgactgatga tggcttcctt gcacaccaca 900
tatacagtgc gcatgcttac agccgggctt ctggagcacc agctgcagcc tggctactgc 960
tttttactgc agaatgaact gcaagttcag catagtggag gggagaggca gaactggagg 1020
agaggtgcag tgaaggttct ctacagctaa gcctgtttga atgatacgta gggtcccccac 1080
caaaagcagg ctttctgccc tgaggacat cttcccactc cctgctcca catgagccat 1140
gcatgcttag caatccaagt gcagagctct ttgctccagg agtgaggaga ctgggagggtg 1200
aaatggggaa atggaagggt ttggaggcag agctgaaaac aggggttgga ggatttcctg 1260
aattagaaga caaacgttag cataccagc aaggaaaatg agtgcagggg ccaggggaac 1320
ccgtgaggat cactctcaaa tgagattaaa aacaaggaag cagagaatgg tcagagaatg 1380
ggattcagat tgggaacttg tggggatgag agtgaccagg ttgaactggg aagtggaaaa 1440

aggagtttga gtcactggca cctagaagcc tgcccacgat tcttaggaag gctggcagac 1500
accctggaac cctggggagc tactggcaaa ctctcctgga ttgggcctga tttttttggt 1560
gggaaaggct gccctgggga tcaactttcc ttctgtgtgt ggctcaggag ttcttctgca 1620
gagatggcgc tatctttcct cctcctgtga tgtcctgctc ccaaccattt gtactcttca 1680
ttacaaaaga aataaaaaata ttaacgttca ctatgctgaa aa 1722

```

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1648 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

tgaccaagaa acagggccta aggatcattt tctcggatgc atcacggctc atcttccggc 60
tcagttcctc cagtgggtgt cgggccaccc tgcagactgt acgcagagag ctacgagagg 120
gatcccagcg gccatgacca ggagccacag gcagtgtctga gccctctcat agccatcgca 180
ctgaaaaatat cccagattca tgagagaact ggccggaggg gacccactgt catcacctga 240
atagaggaaa gatcactcac cagggccaaa gagagtgtc agcgggagat gcttcaactga 300
tgccttcttg ctacctgttt gtgcctctta tgactttgga aaaacaaaag atattttgct 360
tttgggggat agaggggtgg tgggaaaaa aaaaaaatcc atttggtttt ggttttgctc 420
tattcctcca aatgcagcag ggcctttagt tgtctgttaa agctgcacta taatttggtg 480
tctacatttt atcacacaaa ggaacctccc cttttgacaa caactgggct aggcagctgt 540
taatcacaa acattgtgcat cactgtgtgc aagtggagaa atgttctaaa atcacaaag 600
agaacagtgc cagaatgaaa ctgacctaa gtcccagggt cccctgggca ggcagaagga 660
gacactccca gcatggagga ggttttatct tttcatccta ggtcagggtc acaatggggg 720
aaggttttat tatagaactc ccaacagccc acctcactcc tgccacccac ccgatggccc 780
tgctccccc atcccatccc caacatccct gtaccacctt ctctcacatc ttctaaagct 840
ttgtacaaat cacaatgggt cacttccaac aaaatatatc aataggtgtt ttctctctt 900
attttgtaaa tagtattatt ttagctatta agctggatac cttctttcaa attcagccat 960
tcagttgtaa agttgggaag aagtttcttg acaagactct gcaattaaat gottaaaatt 1020
tgagaggggat ccttccttga ttacatcaag tatgttggtg catgggttta tacaagttcc 1080
tcttgagaag gcaaaaagac caccatgtgt gagagctctt tgacttggcc aatagggggc 1140
tatcttaaat cacttgtttg gacacatttc tgatcttatt tgtaaaggct gcaaaaggag 1200
aggatgaaat gctgtaaaaa taggaaatga agtggaagct ggaagaaaat gtaattgggt 1260
gtacagctat gggccagatg gtggagggga ggggtggggc ccctgccggc aagcagagtg 1320
tcacagctgg ctttcctcac ttgggaaaaa ggtactgocg gtctagcagc ctctctgtg 1380
ctcagccagg acacccagcg cgtgggacct gtttgtgtct gttttgcttc cttgggaacg 1440
gcacagtcac tcacctgcc attgocggaa atgacctggg gcactttgac tgtaagcaal 1500
tgcgttattg ctgtagtcaa ggttagtgca agcaaggaaa cattccagc aaggtatttg 1560
tttccatttt ctgtctgtgc ttctgtcaga aacttgctag gacttttagt gccaataaaa 1620

aagaaattcc taatttcaac cttaaaaa

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1648

gcgcgctgat	tggacgcgtg	ggcgaggcg	gaggagagcc	gtgcgcacgg	cgtatgtggg	60
gcggtgtgca	gaccgcgctg	tggcgcaggc	aaggaccttc	aaaataaaca	gcctctacct	120
tgcgagccgt	cttccccagg	cctgcgtccg	agtctccgcc	gctgcggggc	cgctccgacg	180
cggaagatct	gactgcagcc	atgagcagca	atgagtgcct	caagtgtgga	cgatctggcc	240
actgggcccc	ggaatgtcct	actggtggag	gccgtggtcg	tggaatgaga	agccgtggca	300
gaggtttcca	gtttgtttcc	tcgtctcttc	cagatatttg	ttatcgctgt	ggtgagtctg	360
gtcatctttg	caaggattgt	gatcttcagg	aggatgcctg	ctataactgc	ggtagagggtg	420
gccacattgc	caaggactgc	aaggagccca	agagagagcg	agagcaatgc	tgctacaact	480
ctggcaaac	aggccattcg	gctcgtgact	gcgaccatgc	agatgagcag	aaatgctatt	540
tttgtggaga	attcggacac	attcaaaaag	actgcaccaa	agtgaagtgc	tatagggtgtg	600
gtgaaactgg	tcatgtagcc	atcaactgca	gcaagacaag	tgaagtcaac	tgttaccgct	660
gtggcgagtc	agggcacctt	gcacgggaat	gcacaattga	ggctacagcc	taattatatt	720
cctttgtcgc	ccctcctttt	tctgattgat	ggttgtatta	ttttctctga	atcctcttca	780
ctggccaaa	gttcggcaga	agaggcaact	cccaggccag	tgagctttac	ttgccgtgta	840
aaaggaggaa	aggggtggaa	aaaaaccgac	ttcttgcat	taactacaaa	aaaagtttat	900
gtttagtatt	gtagagggtg	tatgtataat	gctttgttaa	agaacccttc	ttcctggcca	960
ctggttgata	gggattgatg	aatgggaaga	gttgagtcag	accagtaagc	ccgtcctggg	1020
ttccttgaac	atgttcccat	gtaggaggta	aaaccaattc	tggaagtgtc	tatgaacttc	1080
cataaataac	tttaattttt	gtataatgat	ggtcttggat	tgtctgacct	cagtagctat	1140
taaataacat	caagtaacat	ctgtatcagg	ccctacatag	aacatacagt	tgagtgggag	1200
taaacaaaa	gataaacatg	cgtgttaatg	gctgttcgag	agaaatcgga	ataaaagcct	1260
aaacaggaac	aacttcatca	cagtgttgat	gttggacaca	tagatggtga	tggcaaaggt	1320
ttagaacaca	ttatttttca	agactaaatc	taaaaccag	agtaaacatc	aatgctcaga	1380
gttagcataa	tttggagcta	ttcaggaatt	gcagagaaat	gcattttcac	agaaatcaag	1440
atgttatatt	tgtatactat	atcaacttaga	caactgtgtt	ctatttgctg	taatcagttt	1500
ttaaaagtca	gatggaaaga	gcaactgaag	tcctagaaaa	tagaaatgta	attttaaact	1560
attccaataa	agctggagga	ggaaggggaa	aaaaaaaaaa	aaaaaaaaaa		1610

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ggaggcgcg  ggagagtagg  gtgctgtggt  ctgagctaga  ggggtgaagct  ggcggacagg  60
aggatggg  tatgcaggtg  atagactaga  gaacaagacc  tctgtctccg  tagcatcctg  120
ggcgagcagt  ctgaatgcc  gaatggataa  ccgttttgct  acagcatttg  taattgcttg  180
tgtgcttagc  ctcatttcca  ccatctacat  ggcagcctcc  attggcacag  acttctggta  240
tgaatatcga  agtccagttc  aagaaaattc  cagtgatttg  aataaaagca  tctgggatga  300
attcattagt  gatgaggcag  atgaaaagac  ttataatgat  gcactttttc  gataacaatgg  360
cacagtggga  ttgtggagac  ggtgtatcac  catacccaaa  aacatgcatt  ggtatagccc  420
accagaaaag  acagagtcac  ttgatgtggt  cacaaaatgt  gtgagtttca  cactaactga  480
gcagttcatg  gagaaatttg  ttgatcccg  aaaccacaat  agcgggattg  atctccttag  540
gacctatctt  tggcgttgcc  agttcctttt  accttttggt  agtttaggtt  tgatgtgctt  600
tggggctttg  atcggaactt  gtgcttgcat  ttgccgaagc  ttatatccca  ccattgccac  660
gggcattctc  catctccttg  caggtctgtg  tacactgggc  tcagtaagtt  gttatgttgc  720
tggaattgaa  ctactccacc  agaaactaga  gctccctgac  aatgtatccg  gtgaatttgg  780
atggctcctt  tgcttggtt  gtgtctctgc  tcccttacag  ttcattggctt  ctgctctctt  840
catctgggct  gctcacacca  accggaaaga  gtacacctta  atgaaggcat  atcgtgtggc  900
atgagcaaga  aactgcctgc  tttacaattg  ccatttttat  ttttttaaaa  taatactgat  960
attttcccca  cctctcaatt  gttttaattt  ttaaattggg  ggatatacca  ttttattatg  1020
gaaaatccat  ttaatttata  caccattcac  cactaaatac  ccccttaat  accccctaaa  1080
atthaagggg  ggttacctta  aagcgatg

```

(2) INFORMATION ON SEQ ID NO. 22:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 675 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
- (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agggaaagag agagagagggc ctagacgaac acaatcacat gttttctttg ctgttcctcc 60
cgggatggggc ctgttttggg gtttgggact ctgaaccgga gcgggggttc ttcgcttgac120
tttgatcctg gtccttaaag gcctttcccc actccctcc cgtgggttca ggggccaagc180
ggccctcct cagagcacgg gcagcacgt ctctggacc cctgtgtgcc agcctctgca240
gacgcagctg gtgggagggg gcatggattt ggaggtggag aagtcactcc tggctcctcg300
agggggtggg ctgtgtgcct agttcagtg gaactcgggg ttggtgaggg cggacaggtt360
tctgaggcct ccctagcctt ctttgtaaat tcacacgaga tagtcaggg ctttccagcg420
cccagcttgg atgataatcc tcgtgtcccc cactctaagg cctccttgag atttclttgg480
ggtctaccac gtcctctgcc tgtctccagg tggtagagga gatgtgggtc ctgtccctct540
cctgggtccc tagggggccc cagggccct ccctgtagct ttagctgacc ccattggtgg600
gggtgtgggg tctgtgcgcg tgctcaggta agcttggggg ctccaggtaa gcggtcccga660
agaacggggg gggag                                     675

```

(2) INFORMATION ON SEQ ID NO. 23:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

agcagagcaa ggttgggttc gctcctctgg cagaacctcg gctctcagga ggtccttggt 60
ccagggaaca gctgcttctc tgggggctgg ggcttctaac ttccctggca gccctcggc120
actaaccag ctggaaccca ggggaacaaa cggcctggag tgccaaacc ttcgtgtcta180
ttttttccag aaaaacgggg gcaatggctg ttgaggagcc catttgggaa gaactggtgc240

ctotaatggg gcaaattgat tctgcagggg gctgcagttg ggcagggaaa attccttcaa300
acaaggggtt ccaccacaac ccaggccccc gcttcaaatt gccagaaaaa 350

```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 746 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ccccccctcc tccggtttt ttttttttat ttaagaaaat ttattttctac ttctacagca 60
gaaatacggg aatggtacag gtttgggcaa atcatacttt atgaaatgga tcctcatacc120
acâtcctttt taatacaggc acgttataac ataattcctg gatttttcaa atccagccaa180
cacggatacc tctgtactc tgttttggcc ttcataagctg cttcctcttt cagacgagct240
ttcttttcta agttcaagct tgttaaaagc tcgtgtcttt gggcagcctt cttgccctca300
ataaccatga agatgcatcc taccaccgtc agggcaatca ttagatagct gatcttcaact360
cgcactctgt tctttgcagc atcaagcatc tccaacgaga cagtctctgg gatttcatct420
tcctttttga agcgacctga ccatacgagg atctttttct gccaatccgt aggtttgtgt480
aaaggcactc tggtgtaagt gcgggatgga gctccgggac tttcctgtgg ttttgtgcaa540
aatccattta ttctcttcaa atcagagctt ctggtaagcc ttagagatga ggaaacatct600
ctttcacata acctaaaaca gcttcctgct gccaggcgca gaccgctgag gctccccatg660
gccacttgct actccgccga ccagcgcaaga acttcgccgg ggacgggtggc gctgggtgagc720
tcaatgtcac ccagcggttg agtggg 746

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 217 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

agtgtatggc agcaaatgag ggatcataac tctcagttta ttgatgatta ttcatoctca 60
gatggaggag tttatccgtc agccacttca gtttgcgtctt aaaacaggag cccacaggac120
ccaagggaact attaaggagg accaggaacc taggtttttt ctttcaaaaa attggcccta180
gcccaataaa tgaaggaaaa aattaggcac cttttttt 217

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 392 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gcg gatccgg cgttctccac tgatcttttc caaggetgta cagacatggc ggcggctttt 60
cggaaggcgg ctaagtcccg gcagcgggaa cacagagagc gaagcagtga ctaccgtaaa120
aaacaagaat acctcaaagc tcttcggaag aaggctcttg aaaaaaatcc agatgaattc180
tactacaaaa tgactcgggt taaactccag ggtggagtac atattattaa ggagactaag240
gaagaagtaa cccagaaca actaaagctg atgagaactt caggacgtca aatatatagg300
aaggggaagag ggtgcagaag ctaagaaaat cgaagactaa aatcagggcc catctgcggg360
ttgcagggga ggcaggaaaa gttgtttttt tt                               392

```

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1796 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

cggctcgaac gtattagttg ttcttaattt ttttcccagt aaaatatgga tcttttaaga 60
agaatttgag aagcaaacia ttacatgtca tgtcaagggg gtagcagatt ccattcgttt 120
tcaatattgc cacaataccc agggattaat gctgccacag gggggcaatc tttatttgtc 180
ttacttccta ccccttccct gttctgcctc ttttaactcag ttaagttgtt ctgtttggga 240
cctggaaaag aacccaaaga aaacctgagt ggacaggttc atttctggaa tgcagaaaac 300
atthttaaag ctagattttt agaataattc caactagcat tctttccatt gatttgaagg 360
ggaaattaac tattataatc tcttgaatcc aaaactggat attaagaact tccccctta 420
ctaagtttaa gacttttgtc atgtggtgag tcaaataaga ccattttgat tgtaaaccat 480
aaaatagttc agcaagtagc ccacagttct ggcctaacag cagacttgct gttttcactt 540
ggtatcctgg agttgggttg ctaaccttaa tttctatgat gttttctaaa atgaaacttg 600
ataaagtaga ccaccagctg caccgtgttt tctgtaaaaag tattgttagt aagtggccaa 660
gagacttgag gaaaatacag attttttgtt taccttggtc ttgttttaag tcttaaaaaa 720
ttaagataa cattataatg tagaatacag atgggacata gtccttgtaa gcttcccttg 780
aaaatgtttt aaatatthag gaagctttta aaagacacta aattgtactc taaaagacac 840
taaattgtac taattgtaca aaggtcaagc caattttatg aaacagtcct acagagtaat 900
atatgtgatg cagtgtaga aggaaaatac tcatctctaa cattatggta ataacattta 960
gcctcttagg agttggagca gggggatggg taattacaga tttgcagact atagaaagag 1020
tttcattttt ttgtgacccc acagagtctc aaatttttat ttcactacct gctagagcct 1080
actgtgaaat cactgctcca ttttgccag tggaggaaat gggcatagag tagagaatag 1140
cttcatatgt ttacacgttt gcatagacta cacacatgtc atgcgtttat ggcaggtagc 1200
tggtatttat tccccaaagt aataatgttg aagtatgggt ctcatcattc ccatacacag 1260
aaacacaaaa cactttgatc ataaaactttt ttcttcagaa gccaaaacta cttgcagaat 1320
aatagagcca ctggtttaat gtttccotcaa gataggtttt agtgtaagct agtattctgt 1380
gtgttcgtag aaatgattca atacctgcag ctggtgaatt aggaattgta tttgttgcc 1440
tttttatatt agatgaggtg caaaaatttt aatgctagtc agtatgcacc accacaggaa 1500
agttagatcc cattagcact tgaaactaca gctttggaaa cttaggctaa gttaatttgg 1560
atthgttact tgattcacct actgaccttt tcttttggtt gaagtgccta tcagcataat 1620
gagctaagtg tcatgcatat ttgtgaagaa acaccctttt tgggtccctt tgggacagag 1680
aggtactcct tgatctttat gaatgacagg ttactgtttt gccttattgc ttaacttaat 1740
gtagtgaat aaagcagaca aagcttgaaa aaaaaaaaaa aaaaaaaaaa tcgacg 1796

```

"179" 179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

gaagaaaaag aggaggaaaa aggtagggag aaataaaggg aggagagaag cacagtgaag 60
 gaaaaaaaaa gtcccttttc gacatcacat tcctgtgttt tccctcagcc tggaaaacat 120
 attaatccca gtgctttttac gcccggaac aaagagacta agccagacta tgggggaaag 180
 ggagataaga aggatcctgg aacttttaaag agggaaagag tgagattcag aaatcgccag 240
 gactggactt taagggacgt cctgtgtcag cacaaggac tgacacacac agacacacga 300
 gaccgaggag aaactgcaga caaatggaga tacaagact tagaaggaca gtcctttca 360
 cctcatccta ctgtccaga aggtaaaaag acacagccag aaagaaaagg catcggtca 420
 gctctcagat caggacaggc tgtggatctg tggcggact ctgaaagctg gagctgcagc 480
 acaccccttt tgtattgtc accctcggta aagagagaga gggctgggag gaaaagtagt 540
 tcatctagga aactgtcctg ggaaccaaac ttctgatttc ttttgcaacc ctctgcattc 600
 catctctatg agccaccatt ggattacaca atgacatgga gaatgggacc ccgtttcact 660
 atgtgtttgg ccatgtggct agtgtgtgga tcagaacccc acccccatgc cactattaga 720
 ggacgacacg gaggacggaa agtgcccttg gtttctccgg acagcagtag gccagctcgg 780
 tttctgaggc aactgggag gtctcgcgga attgagagat ccactctgga ggaaccaaac 840
 cttcagcctc tccagagaag gaggagtgtg cccgtgttga gactagctcg cccaacagag 900
 ccgcccagccc gctcggacat caatgggggc gccgtgagac ctgagcaaaag accagcagcc 960
 aggggctctc cgcgtgagat gatcagagat gaggggtcct cagctcggtc aagaatgttg 1020
 cgtttccctt cgggtccag ctctcccaac atccttgcca gctttgcagg gaagaacaga 1080
 gtatgggtca tctcagcccc tcatgcctcg gaaggctact accgctcat gatgagcctg 1140
 ctgaaggacg atgtgtactg tgagctggcg gagaggcaca tccaacagat tgtgctcttc 1200
 caccaggcag gtgaggaagg aggcaagggt agaaggatca ccagcaggg ccagatcctg 1260
 gagcagcccc tggaccctag cctcatccct aagctgatga gcttccgaa gctggagaag 1320
 ggcaagtttg gcatggtgct gctgaagaag acgctgcagg tggaggagcg ctatccatat 1380
 cccgttaggc tggaaagccat gtacgaggtc atcgaccaag gcccctccg taggatcgag 1440
 aagatcaggc agaagggtt tgtccagaaa tgtaaggcct ctggtgtaga gggccagggtg 1500
 gtggcgagg ggaatgacgg tggaggggga gcaggaaggc caagcctggg cagcgagaag 1560
 aagaaagagg acccaaggag agcacaagtc ccaccaacca gagagagtcg ggtgaaggtc 1620
 ctgagaaaac tggccgccac tgcaccagct ttgccccaac ctccctcaac cccagagcc 1680
 accacccttc ctctgcccc agccacaaca gtgactcgt ccacgtcccg ggcggtacac 1740
 gttgctgcaa gacctatgac caccactgcc tttcccacca cgcagaggcc ctggaccccc 1800
 tcaccctccc acaggccccc tacaaccact gaggtgatca ctgccaggag acctcagtt 1860
 tcagagaatc tttaccctcc atcccggaa gacagcaca gggagaggcc acagacaacc 1920
 aggaggccca gcaaggccac cagcttgagg agcttcacaa atgcccctcc caccaccatc 1980
 tcagaaccca gcacaagggc tgetggccca gccgtttcc gggacaaccg catggacagg 2040
 cgggaacatg gccaccgaga cccaaatgtg gtgccaggtc ctcccaggcc agcaaaggag 2100
 aaacctccca aaaagaaggc ccaggacaaa attcttagta atgagtatga ggagaagtat 2160
 gacctcagcc ggcctactgc ctctcagctg gaggacgagc tgcagggtgg gaatgttccc 2220
 cttaaaaaag caaaggagt taaaaagcat gaaaagcttg agaaaccaga gaaggagaag 2280
 aaaaaaaga tgaagaatga gaacgcagac aagttactta agagtgaaga gcaaatgaag 2340

 aagtctgaga aaaagagcaa gcaagagaaa gagaagagca agaagaaaaa aggaggtaaa 2400
 acagaacagg atggctatca gaaacccacc aacaaacact tcacgcagag tcccaagaag 2460
 tcagtggccg acctgctggg gtcctttgaa ggcaaacgaa gactccttct gatcactgct 2520
 cccaaggctg agaacaatat gtatgtgcaa caacgtgatg aatatctgga aagtttctgc 2580
 aagatggcta ccaggaaaat ctctgtgatc accatcttcg gccctgtcaa caacagcacc 2640
 atgaaaatcg accactttca gctagataat gagaagccca tgcgagtggg ggatgatgaa 2700
 gacttggtag accagcgttc catcagcgag ctgaggaaaag agtacggaat gacctacaat 2760
 gacttcttca tgggtgctaac agatgtggat ctgagagtca agcaatacta tgaggtacca 2820
 ataacaatga agtctgtgtt tgatctgata gatactttcc agtcccgaat caaagatatg 2880
 gagaaccaga agaggggggt tttttttgaa gggggaaaaa cgcccccc 2927

(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 743 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

tccgtggggc tttaaaaaat ggttgtgggt gtgtgggttt ttttgaggtg ggagaggatg 60
tgtgaaaatc ttttccaggg aaatgggttc gctgcagagg taaggatgtg ttctgtatc120
gatctgcaga caccagaag gtgggtgcac actgcatgct tgggggtgcc aagggattcg180
agacctccaa catacttgtc tgaagctcgt gccgctggcc atggcccctc tgccaagcct240
gtgtgcatg ccttggtgc tttagtcaa gaagcctagg ctccagaagca cagcagcgcc300
atctttccgt ttcaggggtt gtgatgaagg ccaaggaaaa acatttatct ttactatttt360
acctacgtat aaagttagg ttcattgggt gtgcgaaaca ccttttttat cacttttaaa420
tttgactttt attttttttc ttccatgctt gttctctgga catttgggga tgtgagtgtt480
agagctggtg agagaggagt caggcggcct tcccaccgat ggtcctggcc tccacctgcc540
ctctcttccc tgcctgatca ccgctttcca atttgcoctt cagagaactt aagtcaagga600
gagttgaaat tcacaggcca gggcacatct tttatttatt tcattatgtt ggccaacaga660
acttgattgt aaataataat aaagaaatct gttatatact tttcaaaatc caaaaaaaag720
tagggagggt aagaaaaagg gcg

```

(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1667 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

agagccaata gcatgggggt tacaaggcaa agatagtcac tcattcaaca catattcata 60
gagctccttc tctgtgccag acactgttct ggaagatagc tagatgaaaa tctttgcaact 120
cacagagctt acatgccagt gagtgaagat cgatgataaa taaagcaa at gcacatcatg 180
ttcacatctt ataagtatat gccaaaaaat gaagccggga aggaggacaa ggcccatggg 240
tgggtgttga ggtrtttaaa grgtggtcag gaaaggcccc actgataagg taacatttga 300
gcaagtctga aaaaggcaag gggatctttg gggctaactt cgggatccct gcactttatg 360
taagaatgta aacctggagt ctcatcttaag aatgatcagc aatacgttta gaacatatga 420
actgaatgaa atggacattt tttcttaatt taagtataaa tccatatgat tatacataaa 480
gttctgatgc attataaaaa gcagccaaat agggccaaag agaaaaataa caggactctg 540
tactggacct aactttatca ttaattaggt aatattttcc tcattttctt actgctgcca 600
ttttctcac cagtattcca gagatggcca tagctcatta ctctaccacc aagaacctaa 660
aaggaaattag aatacagcag aattggcctc agtgaagagc ttaaaattgt tctcctcgta 720
gaactggact attgatcatt accacgtgac gttggctcta ttactttctg ttcccaatgt 780
ccttctagtg gtttgaaaat gttaaaacat ccctaaaatc taaatcatat aatcagaatt 840
ctatagtgtc cactctatc tgtaaagatc atttggaaga ctttagactc tattaatttt 900
aaaaggaata tttattagcc atatgcagaa tttctaata tgatattgta cagcttctaa 960
ttcacttttc agatcagtg ttgaaatggc aattatcagt gttggattta gttccaacta 1020
cttgatttac aaaaatgtac atttagagaa ggttaaaaga aacagtgaga aatgtaaaca 1080
ttcaaaatga taattgaatc tctcagttgt ggggaataatt atcagagaca tgcaactga 1140
aatgtctcac ctttcatctt tttttcttaa ttcataaagt tatcttgtag aatttgatga 1200
gacctccta gtcattctca actggggcgg tgctgtcacc gaatggtgtt tgagagtgtt 1260
ggggctaggg cacatctttt gttgtcacag caactgggtt ggcatttgct gccagtgcc 1320
aggaatagta acattatgaa tgccaggagc agtgtgtcgt gtaaaagtct ccacccaaaa 1380
ggggcagggc acgggtgctc acgcctgtaa tcccagcact ttgggaggcc aagggtggcg 1440
gatcacctga tgtcagggtt tcgagaccag cctggccaac atggtgaaac cctgttgcta 1500
ctaaaaatac aaaaattggc tgggtgtggt gtcacatgcc agtaaccca gctactagg 1560
aggctgaggc aggagaatca cttgaacccg ggaggcagag gttgcagtga gctgagattg 1620
caccactaca ctccagcctg gatgacagag tgagacttca tctcaaa 1667

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 249 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

cgtggtaggc acttcacacg tgtttactga ttgaaaacat tgttgactgt ggcttctatc 60
agagtgtcta ccttttacag ctctgacctt acctcattta atttgctgct tttaatctac120
gggggctgag aatttgtgaa accagtgttg ttagaagtgt atataatctg aatcaataag180
ctctgaatgg gggacaagaa acgctcttat agcacaagaa tgcattggact tcatgacagc240
tcttttgggt                                     249

```

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

aatggaaggt taattaccgg ggcccacctt gagacggaaa aaaattggga aaacgaaact 60
aaaaatgggt ggggtgaatt tctacccaaa gtccagccgt ggtggctgca ctggcacaga 120
atactaaact gagtgtgact attttcaatg caacaaatga aaaaacaaaa tgtgcctgtt 180
taaagcactc agtagagggc tgatgaaact aatttttttt cctttaagac atgcactctt 240
gagtcctaca gtaactgagt gtttgtttag acagcacaaag aaggggtgag agtgcgtctc 300
ctagccttaa tgtgggaggg tagtttcagt cactcatcgg ctttcattat tgtgcagaaa 360

tattagaaaa cctcattgat caattttatg tatttgaata tcagcaaatt gaaattttcc 420
ataattatca ttaatttgta accacatcca gtgtcatgct tactccttag agttcagatg 480
aattctttaa attaaaaaaa aactccatag tactaatttt gtttctttat atagtttgcg 540
tttgatatta gtgcttgcaa ttgtattaaa gtcaaaagct gattttttat gcatacacaa 600
gaatgccact ttttctttta tttcatacca ataattttaa gattgatatg ctaaaaacaa 660
tttgcacagc actaaagcat gagctacttt catctaaacc tgtaaaaaata tgaaagattt 720
ttatatTTTT tcaactggga gaaattcttc ctggatgaaa ttacaaatat gtgtagaata 780
tattttaata aagacttata aaatacctaa ctacaggact taaaatatag attggcgcg 840
agtatataga acaatattcc atataaataa gtttagcctt tataaaaaatg aagttgcagg 900
ctgacattac attctgtact tactaagtgt caacagccct tacaacatt aaatgtaaat 960
ggtttcaaat ggtcagcgtt gtttaaagt aatcatgtta ttttattcat tgttaatgct 1020
ttgatgaaaa ggctttatat gcagtagatc tacgaaaata ttgttcatac tgatcagaat 1080
taaatTTTgt tagagcagag ttttaaaatg aatgtaaata gcactaaacg ttttctttct 1140
gcaacctgta cttacagatt cttcctgtaa actaaataaa aaaaaaatga tagtgcaaaa 1200
aaaaaaaaaa aaaaaaagag acggagagag gagaaagagg gcgtggg 1246

```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 215 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

gggaagcatt ttggatatga tgcaggaaat ctotctctgg agtcaaaaagt tccaagagg 60
tgctgtatTT ttaagaaatg gagtttatTT aaataatagt taagcttggt cccatgttgg 120
ccgggcaact tttttcaatg gtgcttatta gaagaagtgt tttcatctgg tcaatttaag 180
gaaataaaaac taggaaatgg agaggggggg agaga 215

```

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 734 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

gctgccggggg gcctgggggct cggcgctcgggt ccccggggga tgtggagagc tggcagcatg 60
tcggcccgagc tgggagtcgg gtgcgcattg cgggcgggtga acgagcgcgt gcagcaggct120
gtggcgcggc ggccgcggga tctcccagcc atccagcccc ggctagtggc ggtcagcaaa180
accaaacctg cagacatggg gatcgaggcc tatggacatg ggcagcgcac ttttggcgag240
aactacgttc aggaactgct agaaaaagca tcaaatccca aaattctgtc tttgtgtcct300
gagatcaaat ggcaacttcat tggccacctc cagaaacaaa atgtcaacaa attgatggct360
gtccccaatc tcttcatgct ggaaacagtg gattctgtga agttggcaga caaagtgaac420
agttcctggc agagaaaagg ttctcctgaa aggttaaagg ttatggtcca gattaacacc480
agcggagaag agagtaaaca tggccttcca ccttcagaga ccatagccat cgtggagcac540
ataaacgcca agtgtcctaa cctggagttt gtggggctga tgaccatagg aagctttggg600
catgatctta gtcaaggacc aaatccagac ttccagctgt tattgtcgt cccggaagag660
actgtggtaa aaagctgaac atccctgctg aacagggttg gctgatcatg ggcattgtccg720
tctgtaaaact gcaa

```

734

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 314 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gctgctgggg agccactgaa ccaaccggag acccgctggt cccacgtgaa gcagctgtcc 60
tggtgtggag gtacagagct agaccagcac tggccctcc agcccctgg tagcctctgc120
tgcaactgaa ctggcagctt ttgccgctgc ctttagctct gcatgtatgc gccctgaagg180
ttctgcctct ctgttttgga atcgccctcc cctcctcatg tttggggacc tgcaagggtg240
tgaggcacgt gagggcatcg ccatgcgtat ttacagggc tctttctctg gactgtcttc300
aaagggatga cttt                                     314

```

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1839 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

gcgggcgagg	gcggaagcaac	agagcgggcg	ggagtaaggc	ggagtgaag	gaggagcttg	60
atggaagcgt	gcgagaagg	gcgtaactga	tttggaacc	agaggaaagg	cgctgttttc	120
accgaattag	aatcgcgga	aaatagagaa	gagttgttt	gaaggctctg	cgagatcgag	180
tgagtacggc	tcgccaagt	ggagcgctct	cgcatagac	acagcaacta	ttcagctgcg	240
aggggacggg	agaggtggtg	agcactctcg	cgagatttga	aggagcggcg	gaggccagag	300
ggaggagagg	accggaagtc	cttcatctca	agcatccaat	gctgaaacgg	gcctgatttt	360
ctctaccgga	agcccttttc	ctagaggtcg	gaacacggcc	cacctagcag	gaagtccac	420
ctccttgagc	ttccgccacc	ttcccgaa	ttttctgtca	cctgtcttag	gctccgtccc	480
ctttccgctg	tttatcccg	taccagaaaa	ggatacattt	agtgcctccc	accagctccc	540
actaaacggc	cttcccgctt	cctgtggttg	tggccgctgt	gctgtgggga	gcgccccga	600
cccgggggct	cattcgagcg	acctcgga	acaatgccag	catggacttt	gcagaccttc	660
cagctctgtt	tggggctacc	ttgagccagg	agggcctcca	ggggttcctt	gtggaggctc	720
accagacaa	tgccctgcagc	cccattgccc	caccaccccc	agccccgggtc	aatgggtcag	780
tctttattgc	gctgcttcga	agattcgact	gcaactttga	cctcaagggtc	ctaaatgccc	840
agaaggctgg	atatggtgcc	gctgtagtac	acaatgtgaa	ttccaatgaa	cttctgaaca	900
tggtgtggaa	tagtgaggaa	atccagcagc	agatctggat	cccgctgtga	tttatggggg	960
agagaagctc	cgagtaccctg	cgtgcctct	ttgtctacga	gaagggggct	cgggtgcttc	1020
tggttccaga	caataccttc	cccttgggct	attacctcat	ccctttcaca	gggattgtgg	1080
gactgctggt	tttgggccatg	ggagcagtaa	tgatagctcg	ttgtatccag	caccggaaac	1140
ggctccagcg	gaatcgactt	accaaagagc	aactgaaca	gattcctaca	catgactatc	1200
agaagggaga	ccagtatgat	gtctgtgcca	tttgcttgga	tgaatatgag	gatggggaca	1260
agctgcgggt	actccctgt	gctcatgcct	accacagccg	ctgcgtggac	ccctggctca	1320
ctcagaccgg	gaagacctgc	cccatttgca	agcagcctgt	tcatcggggg	cctggggacg	1380
aagaccaaga	ggaagaaact	caagggcaag	aggaggtgga	tgaaggggag	ccaagggacc	1440
accccgcttc	agaaaggacc	ccacttttgg	gttctagccc	cactcttccc	acctcctttg	1500
gttccttagc	cccagctccc	cttggttttc	ctgggccttc	aacagatccc	ccactgtccc	1560
ctccctcttc	ccctgttatc	ctgggtctaat	aacccccac	acatacacct	ctggtgacct	1620
atttgcacag	accgtcgtct	tccttcag	cttctgaggg	ataggggaca	ttccatccca	1680
agcttctctc	ttaccacac	ctatcctttt	gaggggcttt	gggggtgggg	tggggcaagc	1740
agagggtactg	ggtcttcact	ctttgggcta	ataaaattgt	ttctttgtgg	actaaaaaaa	1800
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			1839

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1931 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cagccgccgc ccacccctct ttgtgtgctt tggaaagccg cggagctggt ggtggctaca 60
gttgggtgtt ggggcttagg cgagggacgt taccgggaag ttgcaggcgg gaggactctt 120
ccccatccag tcacctgaca ggtcacaaac atgtcagaca aaagtgaatt aaaggctgag 180
ttggaacgta agaagcagcg actggcccaa atcagagagg aaaagaagag aaaagaagaa 240
gaaaggaaaa aaaaaaagaa agaccagaag aaggaagctg ttgctcctgt gcaagaagaa 300
tcagatcctt aaaaaaaaaa gagagaagct gaagcattgc ttcaaagcat ggggctaact 360
ccagaatccc ccattgtccc tctctctatg tctccatcct ccaaactctgt gagcactcca 420
agtgaagctg gaagccaaga ctctggagat ggcgccgtgg gatctagacg aggacctatt 480
aaacttggaa tggctaaaaa cagcgaagtc gactttcctc ctcgagaaat tgtcacgtat 540
acaaaggaaa ctcagactcc agttatggct caacccaaag aagatgaaga ggaagatgat 600
gatgtagtgg ctccctaaacc acctattgaa cctgaagaag agaaaacttt aaagaaagat 660
gaggaaaaat atagtaaagc tccccctcat gagctgactg aagaagaaaa gcaacaaatc 720
ttgcactctg aggaattttt aagtttcttt gaccattcta caagaattgt agaaagagct 780
ctttctgagc agattaacat cttctttgac tatagtggga gagatttggg agacaaagaa 840
ggagagattc aagcaggtgc taaactgtca ttaaatacga aattttttga cgaacgttgg 900
tcaaagcatc ggtgtgttag ttgtttggat tggtcattct agtatccgga gttactcgtg 960
gcttctata acaacaatga agatgccctc catgagcctg atggtgtggc ccttgtatgg 1020
aatatgaaat acaaaaaaac taccacagag tatgtgtttc actgccagtc agctgtgatg 1080
tctgccacat ttgcaaaatt tcatccaaat cttgttgttg gtggtacata ttcaggccaal1140
attgtgcttt gggataaccg tagcaataaa agaactccag tgcaaagaac tccactgtcal1200
gcagctgcac acacacaccc tgtatattgt gtaaattgtt ttggaacaca aaatgctcac1260
aatctgatta gcatctctac tgatggaaaa atttgttcat ggagtctgga catgctttcc1320
catccacagg atagcatgga gttggttcat aaacagtcaa aagcagtagc tgtgacatct1380
atgtccttcc ctgttgga tgtaacaac tttgtgtgtg ggagtgaaga aggttctgtg1440
tacacagcat gccgccatgg cagcaaagct ggaatcagtg agatgtttga ggggcatcaal1500

ggaccaatca ctggcatcca ttgtcatgca gctgttggag cagtagactt ctcacatctt1560
tttgtcactt catcgtttga ctggacagta aagctttgga caactaagaa taacaagcct1620
ttgtattcat ttgaagataa tgcagactat gtttatgatg ttatgtggtc acctaccac1680
ccagccctgt ttgcctgtgt ggatggcatg gggagattgg atttgtggaa tctcaataat1740
gacacagagg taccaactgc cagcatttct gtggagggtg atcctgctct taatcgtgtg1800
agatggaccc attctggaag gggaggtggt tgtggcggga ttctgaagga caagttttgt1860
tattttgcga tgttgggagg agcagtttgt tggccccccc aatgatggat tggcgacggt1920
tggcccgacc c

```

1931

(2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

agttaccatt gcctttttctg tctcgtgccg gttttggttt gctgaaacta gtccaaaaca 60
ggaaatttaa cagacagcca cagccaaaga gtgtcatgtg aattacaaga aatagagccc120
atthagggaa agatagaact agaaaggctt ttcattataa ttccatgttg aacaattgag180
tcatagcttc ttatcttgga ggaaggacac aattcaaagg ggcagtaagg attttgtaaa240
acgtggcatc cataatttac tatggagcaa gtgccacat ctctaggaca ttaa      294

```

(2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

tttttttttc tcattaacaa agcagtcfaat tccctttatt tttaaaattt tatgtacaca 60
tatgaatgat ctgtataatg tacattcaat atagaaagct ttatatattt gatagtgtat120
agaacatttc acaattacac tcatctttta cataacatct tgacatccat ttttaaattt180
ttttgcacaa gctccttttc attcaatttg gtaaagccag ttatacatat taatgtgtac240
tgtgagcttt cagaagggtta atgattgagg atgccagtga aggggtgcagg gacaaaacct300
aatagtcttg gatgggtggg ggaggatggc cacgcagact tgatgcagga gagggaaata360
ttctttcctg gggaaaagtg acttagccca atttttggtg actgtagctc aacctacag420
tcatgctagt tcaaaaaaaaa aattacaaaa actaggaaga aagttttgtc tttttgattc480
acagttttgt aaacagatat aaaggaacaa atgtgcttac atacaccaag aaaaaaaaaa540
ttcttggtga cccacttatg ttgatccaca gagggtcttc ttataatgtg atacaattag600
gatcactgac tttttttcct aaaaatatat ttatagaaaa aggaataaca ctgtcatgaa660
accaggagaa aggcagtaag agtttgcttc aacgtatcag ctggaggaat gtggacttgg720
cactggcctt tcagcgctta ttgtctctcg tgaatatctc aagtctgata gccaaaggtcg780
cctgcctcat ggtctacagg aggtggcagg ttagacatga ctgatgtaga tgtactgcgg840
taaggtagcc agcaactcca ggtcctgctt cagagagcta ca
882

```

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 934 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

ctcgcgccgg acacagggag cagcgagcac gcgtttcccg caacccgata ccatcgga 60
ggattttctcc gccctcagccc aacggggagg gctagttgca catagtgatt tagatgaaag120

agctattgaa gctttaaaag aattcaatga agacggtgca ttggcagttc ttcaacagtt180
taaagacagt gatctctctc atgttcagaa caaaagtgcc tttttatgtg gaggcatgaa240
gacttacagg cagagagaaa aacaaggagc caaagtagca gattctagta aaggaccaga300
tgaggcaaaa attaaggcac tcttggaag aacaggctac acacttgatg tgaccactgg360
acagaggaag tatggaggac cacctccaga ttccgtttat tcaggtcagc agccttctgt420
tggcactgag atattttgtgg gaaagatccc aagagatcta tttgaggatg aacttgttcc480
attatttgag aaagctggac ctatatggga tcttcgtcta atgatggatc cactcactgg540
tctcaataga ggttatgcgt ttgtcacttt ttgtacaaa gaagcagctc aggaggctgt600
taaactgtat aataatcatg aaattcgttc tggaaaacat attggtgtct gcctctcagt660
tgccaacaat aggtctttttg tgggctctat tcctaagagt aaaaccaagg aacagattct720
tgaagaattt agcaaagtaa cagagggtct tacagacgtc attttatacc accaaccgga780
tgacaagaaa aaaaacagag gcttttgctt tcttgaatat gaagatcaca aaacagctgc840
ccaggcaagg cgtagggtta ttgagtggta aagtcaaggt ctggggggaa tgttggaact900
gtttgaattg ggggtgttcc gcttaggaag gttc

```

934

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ctcgtgcggg tcaattatga gttcctttat ttattggtga gaaagattag caagtatgac 60
gtatgcaagg aatagaagtt atgtaccgag tggttaaagg ttggggggat atggagatgg120
atgagaggga gctgtctggg aaggctttgc ttcaacttga ttagagtagg gttgcgtgag180
gaaatagggt tgtagaatga gaatgagggt catgacagcc tctacaaaa c

```

231

"BIBL" 01/02/2000

(2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

cgatcacggtt ttcacatgat gctcacgctc agggcgcttc aattatccct cccacaaaag 60
 ataggtggcg cgtgtttcag ggtctctcgt ctctctccta cagaaaagaa aaagaaaaaa120
 atgtcattag aagaggcgta acacgtcagt ccgtccccag gtttggtgtt cctggagtgg180
 ccgaaagaga tcagttctaa cctgctctgc aggaataacg gtcctgcctc ccgacactct240

(2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

```

agagcagatc agaggcaggg ggaaaagcac gcagagggag gagctgaaga gctgagaccc 60
ggagccaggg acagcttaat gaagacaaac tgaaggggaa actgagatgc ttagaaagcc120
cagctataca actctaccca gaaatacttc ccttagggaa tgtaaaaagt actactggag180
atggaagagc agaaaaacag ctatgggcag aaggccaagg ggtgatag      228

```

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

aaaaaaaaa aaaaaagagt taatctagga gataatgaat ggcctagtag tagataatat 60
atggccccc aagctcttga cttctgtcct tggggaaaagc cattttgtta accacactag 120
tgagatttac atgatgctta atggagaaca gagaagatct tgttgcaaaa ggtgtattaa 180
atatttgtgc tgtttctgta tgagattgag aagcttttcc cacctctcac ccctatttcc 240
tataaggata tccagagaag ccaaactgtt ctgtgggttt gggaatggtc atttcccggt 300
aaaatgcac tggatcgatg actaaacctg gcccttttct ctgggctgta gtgaagccgc 360
attttcacgc tggctggcag tgtgctgaga gcctcgaatg ctctgcggcg tagtgccctt 420
ctgccctgcc tgacgatgta tcgaaaagat gagagtgaag gagactttgt gcagcaggaa 480
acgggtaggt gaggtgttgg gcagttgtgg gaacttctga gagtattaca gagtggtaga 540
atcggtaaga actctgattt ggacttcgct ttggtggaac tgtgtgccta tacctgcctg 600
tgtgtgtgca agtgtgcagg ttcttttgta tgtatgtgta cgtgtgggaa cctgtgtttg 660
tcatattttt cttcatttca caaaggcttt ttttgaagca gtggcagtat gcctttgttt 720
caagaacaca tgaaattctt ttaacaccag attagtgtgt taccocaaat gaacggttct 780
agccctctat taagaaataa agggaccata agcatttttg ctgcttatgg ctgtgtgtta 840
ctacttacaa gactcttgaa aattatacag aactttgcct tcttttttta atgtcttcca 900
caatgttttg actgattata accctgtttc ccctcagaga agagctatgg ctcagggatc 960
tgtgttgact ctggcattta gtggctttgt gaaggaaaga aaccattaaa tgacctgaca 1020
aaaactgact catgtcttta aagtagttga agccactttt aggaatgtta ctctcggttg 1080
cttttgtcta attctaattg gcttaaagcc aagaaaacca tagtataaat cttttttgtg 1140
taccctatgg ctagtgtttt aaatgggcag ttccgtttgt gataaagtat ccagtcactt 1200
caggtttccg tggaaaggtt ttattgggg 1229

```

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

gaggccggga gtggaacccc ctcttttgag aaggttgccct gactcagaga cacagaaacg 60
ggtccaggga tggggagaga tgtggagtga gggaagggtt gcatttgaga aaggaagtct 120
gagaacacac tgggacattg taacacattt gaaccatctt ctgatagaaa ggtgttgccc 180
tcctaataat gggaggtcag ggccagggtc tcgggcatag ggagagggtc c 231

```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

tttgccatca ttacaaattt catagaatta ctgtgaaggc ctttctagtt gagatggttg 60
ggtatttggg attctaattg ttaaccccag aagaaggtaa tttagcttgt atttatttaa 120
aaccatttta gctttttact tatatctggt agaattccag tgatcatcct aataaggat 180
atttcagaat aatttttttt tccttcagaa taacttagaa tcagatgcta taagggtcc 240
taggagcagt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatatta 300
aaccaagagg ccattttcaa tatgattttt tgtttctttt taacttggtta agtccctaag 360
agattacatg ctagggtctg agtcattttc attgtagata atgatggccc acacagtcac 420
cttcaactat ccacataagc taggctttcc gcttttgcca cggacagtgt gaccaagata 480
tttcagagat aaataaccca ccacaacctt ggtaattcct cttttcttct taagctccag 540

gaagcgaaaag cagaaggact cttttcagac tgccctctgt agcctacatt gcagctttcc 600
aaaacaggca gctagcactg ggaaagccca tgtgttgacc ccatattttt ctgagggtct 660
tcttttccat ggtgttactt tattatcaga aagtaaattc agaaaacagg tcttgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tccagcccca gaacttgtaa ggattttgtt tgaacactga gcagatgcct 840
ctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ctgcagtctg ctagggtatg gccttcttat cccactctcg cacacatccc agtctagtct 960
ttgccttcac agagtcctcc ttgacacccc tgacttaatg atagttgctg ttttgagta 1020
gaattgatca ggtttaagtc atcctgctca ggttgggcat agtggctcat gcctgtaatc 1080
tcagcacttt gggaagccaa agtgggagga ttgcttgagc ccaggagttc caaaccatcc 1140
tgggcaacag agggagaccc tgtctctacc aagaaaaaaaa aaaaaaaaaa aaagttaaaa 1200
aaacaattag ctggacctgg tgggtgcacac tcagtaggct gaggtgaaag gattccttta 1260
acatgggaga ctgaagatgc agtgagccat gaatcagcaa ctgcacacca gtatgagaga 1320
aaaagtggaa ccctatcaca

```

1340

(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 226 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```
gccagatttc cgggggttttg cggggcccgcc gatgttttcc agaggttttc aagtgggaag 60
aggagagcga caaggtgaaa atgcccogtg cgggggcgtc cagcggagtc ctgccagctg120
tcgggcgggtg ggggtggacgt ctgatttatg aaggtgcca tccacctatc tgagtacctg180
acttgtaggg actgacaact acagcatcag gtacaaagtt gttctt 226
```

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 611 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

gcagctgcag cggcagcagc ggcagcagag gcagcagcag tagccaccac tccgccgagg 60
ccgcaacccc ggctcggcct ccccgaggcc cgcgctgcc gcagtcattg ctgctgatgg120
ggtggacgaa cgctcgctc tgctgtcagc atccactcc ggaaatgtca ctccaccgc180
cccaccgtac ttgcaagaaa gcagccccag agcggagtcc cacctccata tacagccatt240
gccagtcacg acgccaagtgg tattccagta ataaactgcc gtgtgtgcc aatcactaatc300
aattttgatg gcaagcttca ccagcatgtg gttaagtga cagtttgcaa tgaagctacg360
ccaatcaaaa acccccacac aggcaagaaa tatgttagat gcccttgtaa ttgtcttctc420
atgtgtaagg acacatctcg gcgaatagga tgcccaagac ccaactgtag acggataatt480
aaccttggcc cagtaatgct tatttctgaa ggaacaacca gtcagcctg cattgcccac540
tccaaccag aagggtacaa gggctgtgtg ttggggcacg gttggggaac acattccctt600
tgggatggga c

```

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 689 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

gccgaccgga cgcagggggc tggcgggaac gtgaagctcc gcggtgcctg atggggccgt 60
tgggcggcgg gtagctgttg ctgttggggg accccctcat tcctgccgct gccgtccctg120
ctgcctcatg gcggccatcg gagttcacct gggctgcacc tcagcctgtg tggccgtctc180
taaggatggc cgggctggtg tggttgcaaa tgatgccggt gaccgagtta ctccagctgt240
tggttgcttac tcagaaaatg aagagattgt tggattggca gcaaaaacaaa gtagaataag300
aaatatttca aatacagtaa tgaaagtaaa gcagatccctg gccagaagct ccagtgatcc360
acaagctcag aaatacatcg cggaaagtaa atgtttagtc attgaaaaaa atgggaaatt420
acgatatgaa atagatactg gagaagaaac aaaatttggt aaccagaag atgttgccag480
actgatattt agtaaaatga aagaaacggc acattctgta ttgggctcag atgcaaatga540
tgtagttatt actgtcccggt ttgattttgg agaaaagcaa aaaaatgctc ttggagaagc600
agctagagct gctggattta atgttttgcg attaatcac gaaccgtctg cagctcttct660
tgottatgga gttggacaag actccccta

```

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 560 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

agaaaatgga cgctgacatc aatgtcacaa aagcggatgt tgaaaaggcc cgacaacaag 60
ctcaaatacg tcaccaaatag gcagaggaca gcaaagcaga ttactcatcc attctccaga120
aattcaacca tgagcagcat gaattattacc atactcacat cccaacatc ttccagaaaa180
tacaagagag cggaggaaaag gaggattgtg agaatgggag agtccatgaa gacatatgca240
gagggttgatc ggcagggtgat cccaatcatt gggaagtgcc tggatggaat agtaaaagca300
gccgaatcaa ttgatcagaa aaatgattca cagctggtaa tagaagctta taaatcaggg360
tttgagcctc ctggagacat tgaatttgag gattacactc agccaatgaa gcgcactgtg420
tcagataaca gccttttcaa ttccagagga gaaggcaaac cagacctcaa atttggtggc480
aaatccaaaag gaaagttatg gccgttcac taaaaaata agcttatgtc ccttttaacg540
ggggggcccat tcagcttcag                                     560

```

(2) INFORMATION ON SEQ ID NO. 56:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 851 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

gaagaagagt aagaaggaca agaaggccaa agctgggtctg gagagcgggg ccgagcctgg 60
agatggggac agtgatacca ccagcaaaag aggtagaatt ggtttctgag tagtgaaggc120
cacttgaagc tggaggagaa actaaagcct tattgagaaa acatgtttata gatccttttg180
ttgctgagag agtggaacat aggtcctaga caggggtgaag agttctggca catttttagct240
gctactttga gacctcgggtg atgttacctg gtgtgggtcat cccatcttgt cctgttttaa300
ggatatgggt ggtgaaagat gaaagaggca gagtttatcc caatgacttc tctgtttgag360
ttgggaagcc tcaccttcag acccagtaac tgtccgcagc tgtctgctag tggttgtctt420
aacatcgtag tcctagtttg catTTTTTaa atccccctctg tttaaaaggt ttgtaaaaca480
aaaacaaaaa actaagtctg ctcaagtgaat tgctgtagaa ccctaaataa gtggtagaag540
agtgtcactg aattttgtct ctgaattcag tataactgag ttttgtccat gctggtgtct600
gggttatagg cctgatgggc ctggtagttt tccatcttgt tctggcctag aggtcagtc660
tttgcacttc ctcaaagctt gtgtacagtg ctcacctaaa tccatctgac tacttgttcc720
tgtgccctct tgttttaggc ctcgtttact tttaaaaaat gaaattgttc attgctggga780
gaagaatgtt gtaattttta cttatttaaag tcaacttggt aagtttttaa aaaaaaaaaa840
aaaaaaaaa a                                     851

```

(2) INFORMATION ON SEQ ID NO. 57:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

cttaccaaca gcctttctgc taagttctgt tttttggata tttatgactt ggttcatctt 60
atTTTTtTcct gatttagcag gagcccttt ctatttcagt ttcattttca gcatagtagc 120
ctttctatac tttttctata agacttgggc aactgatcca ggcttcacta aggcttctga 180
agaagaaaaa aaagtgaata tcatcacccct tgcagaaaact ggctctctgg acttcagaac 240
atTTTgtaca tcatgtctta taagggaagcc attaagggtca ctccactgcc atgtatgcaa 300
ctgctgtgtg gctcgatatg atcaacactg cctgtggact ggacggtgca taggttttgg 360
caaccatcac ttttcatat tcttcttgtt tttcctttcc atggtatgtg gctggattat 420
atatggatct ttcattctatt tgtccagtca ttgtgccaca acattcaaag aagatggatt 480
atggacttac ctcaatcaga ttgtggcctg ttccctttgg gttttatata tcttgatgct 540
agcaactttc cattttctcat ggtcaacatt tttattatta aatcaactct ttcagattgc 600
ctttctgggc ctgacctccc atgagagaat cagcctgcag aagcagagca agcatatgaa 660
acagacgttg tccctcagga agacaccata caatcttggg ttcattgcaga acctggcaga 720
tttctttcag tgtggctgct ttggcttggg gaagccctgt gtggtagatt ggacatcaca 780
gtacaccatg gtctttcacc cagccaggga gaaggttctt cgctcagtat gaagaaaagc 840
aacccaaaac tctcaatctg atttgTTTTT gtttatgtcg atgccctgta gtttgaaagt 900
gaagtaaaag tttagaattc acctaaagtc aaaggaaaaa acgtggTTTT taaagccatt 960
aggtaaaaaa agttctcaat aaaggcatta caatttttta ggtttagaaa gatggacttt1020
tttgataaat cttggcagac atctaaaaaa aaaaccatat ttttcacaag aaaatgcaag1080
ttactTTTTT tggaaataat actcactgat tatggataaa atggaatatt ttcagatact1140
atattggctg tttcaaaaata gtactattct ttaaacttgt aatttttgct aagttatttg1200
tctttgttgt atctataaat atgtaaaaaa tatTTTaaata gatgtacctg ttttgctttt1260
acacttaata aaaaattttt ttttgtaaaa ggaaaaaaa aagaagagga aaaagaagag1320
aaaggagagg ggaagaaaag ggagaaggca agga
1354

```

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 268 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

cgtgatctct cctcagtaaa accaaggtgc atttttctgg acccacctat cttggggggtg 60
attaggagta gaggggttgta aatacttaaa atttttttcc tttctgatat aattattgat120
ctccctctag aagtcctgtc gtctttgctg gagaattttt atttaagcat ccttttgtag180
aagaatctct aatgtccctt tttcatccag atctacactt gatgaatcct aaagctattt240

ctacacagtt cctttattca gttttccc                                268

```

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 752 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

tgacaaaaga aatggaataa tttcaaaaaa gttaagtctt gagaagacaa ccctgaaatc 60
tattttgaaa agaaaaggca ccagtgatat cagtgatgaa tctgatgaca ttgaaatttc120
ttccaagtca agagtaagaa agagagctag ttcattgagg ttttaagagaa taaaagaaac180
caaaaaagaa cttcacaatt ctcccaaaac aatgaacaaa acaaaccaag tgtatgcagc240
aaatgaggat cataactctc agttttattga tgattattca tcctcagatg agagttttatc300
cgtcagccac ttcagtttct ctaaacagag ccacagacca agaactataa gagacagaac360
tagtttttct tcaaaattgc ctagccataa taagaaaaat agcactttta ttccaagaaa420
accaatgaaa tgttcaaattg aggaaagttg ttaatcaaga gcagtcgtat gaatcaatgg480
ataaattttt agatggcggtt caggaagtgg cttatattca ctcaaaccag aatgtaattg540
gatcgagcaa agctgaaaat cacatgagcc gatgggcagc acatgacgta tttgagttga600
agcagttttc acagctgaca gctaacatag ctgtttgcag ttotaagaca tataaagaaa660
aagtggatgc agatacattg ccacacacaa agaaaggcca gcaaccgagt gaaggcagca720
tttcaattcc tctttacatt tcaaatcctg ta                                     752

```

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

"EST" data-bbox="38 365 60 588"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

gaactccaag ttagtggatt gcagaatgga aacttggctt ttgcggcact gggtgagttt 60
tagtttgtgt gtgtcttgct ggggggtggt gatgattgtc tcagcactca cgcactgcac 120
aagatggcag caggatacag cactgcacaa gatggcagct cctctgcagc ttcctcctca 180
gcctccctcc ttgcaccccc acaggttttg cttgtggttt ttgtcatcag taacctactg 240
cctgagatca tgatctctta aaagatgaga ctctcggaag ggttgattgt atgcgtcagt 300
gagccttcta tcaccttctg gaacaaagtc acttgaaatc tcttgatgag attaaggagt 360
ttagtgttac taagaaaatc tgctttgggc cgcagcagtg ctgggtgttc tcagacctga 420
ctgagggaagt tagctgcggg ctgccctgtg ggttggtgct tcaggaggaa tccagagaag 480
tgttcagatg ccccccttgg gctcctttct tatcttaatc agctctttaa atagctgccc 540
atctcctgtg attgcacaac caagcacttt gacatttgca ccttaggaga ggcagatgtt 600
aaaatggaat ccaaagacca cctagggcgg ggctgggtgg gagatgggag ggccaactgc 660
gagctgctcc acttctcagc tctccctgct cctgcagccc tgggccagac aaggccagaa 720
ggtttcaggg gcatttgaca tcccctcctg gttctcacca ggaaaacatc caaagctttg 780
gaggaaacag gccctgcccc tggctcctta aatgccccgt ctctttgtaa actgatattc 840
agccagcaat gcctaagact ttgttaagat cattttctact gcttttcttt ctgcttcaaa 900
cacacagttc gtctctgagg aaagtaaaat aaatggaata agagtaaatt gggtaaggag 960
atatccaaag ctaccagtc ccttgaccca gcacagttgg ccgaccctg tcactccctg1020
gctgtcgctg cttctctgtg ctactgaag ggtgagccag gccagtgtt cccagcccc1080
tgggcctggt cactacacag tggaaaacag acaagcggcc ccttcccca atcccaagag1140
tgtcttgctg cttggtgggt gctcatcgca atgttctgaa ggctccaggg ccactttgtt1200
tgtaagtatg atctgggctt caaaatacca tagtagctgc ttgataaaat tctaaaaata1260
tctggttctc tattatgtaa acactattac agtcaccagt gtgtgaagac tcttgagtct1320
ggttctcata tcagagtcac catttttctt cctgtggaat aaaatgcctt gtggacttcc1380
caaaaaaaaaa

```

(2) INFORMATION ON SEQ ID NO. 61:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

cgtatctgtc cggacggaag caggaagcgg gagcgtagg gccacgcctg cggcgctgct 60
ggttgaggct gtgtgggtgg gggacgggccc gaggcgatgg cggagaagtt tgaccaccta120
gaggagcacc tggagaagtt cgtggagaac attcggcagc tcggcatcat cgtcagtgac180
ttccagccca gcagccaggc cgggctcaac caaaagctga attttattgt tactggctta240
caggatattg acaagtgcag acagcagctt catgatatta ctgtaccgtt agaagttttt300
gaatatatag atcaaggctg aaatccccag ctctacacca aagagtgcct ggagagggct360
ctagctaaaa atgagcaagt taaaggcaag atcgacacca tgaagaaatt taaaagcctg420
ttgattcaag aactttctaa agtatttccg gaagacatgg ctaagtatcg aagcatccgg480
ggggaggatc acccgcttc ttaaccagct caccctccct gtgtgaagat cccctgggac540
tgcatgctgg cgtgaggctg ggactgctg tgctgacgcc accttcctgc tgagggtgga600
ctgggcccctg gacacacccc tcagcccctc tgcctcatt gtttgccctc atgggaccga660
ggggctggag gagaggcgga gtgtgccc aa ggttcaaga ggttggttg ggtgaaatgg720
gtttgt

```

726

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 681 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cdna library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

ggctgagaaa aatgggggga gacataacac ccacgaatga aaatacagat ttaagagaag 60
gaaccagtaa agtaggagac agatgtgaag gaaatggaaa tgaggcaaga ggacattgga120
agagagaagt ttgtgtgcca ggagccaggt ctggagcacc agtgtgaggg agttcaggta180
ggctgggccc gtgcccctag gtagggacaa gggaggctgg gtagccaggg ctggtgctta240
aaacccctga ggccatgagc tcattggctg cctttgtagc atcctgtctt cttctgtgct300
gcttggtttg atctcatctc acctggattc aaagggttaag gtgggcatgg gtcttggggc360
tgacacccac caaggatgac ctgtggactg ccacgggatg ctgaacaggg agatgaaagg420
aggtcctctt accatacccc tctgccaacc cccagtagg ccactgttct gactttgttt480
ccagaatata cagaaatcca aaggggctgt tgctgaacag tctgcaggac cagtgcagc540
acctacctgt tgtcccaagg catacaaagg aggcctcaac gctcatgctt ctctaataa600
gccctaccaa gacagacaga aaaggaaggg gtagaggaga aggttgaagc tgtggagtta660
gactctgctt cattcctgaa g

```

681

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

gggccacact gagcagattc tttggtagaa ttttcaactt gagactaaca caagtatttc 60
cttttctggt cagttctcca aatgacaaga agtctttttg ctcaattgaa ggggaatgga 120
atggtgtgat gtatgcaaaa tatgcaacag gggaaaatac agtctttgta gataccaaga 180
agttgcttat aatcaagaag aaagtgagga agttggaaga tcagaacgag tatgaatccc 240
gcagcctttg gaaggatgtc actttcaact taaaaatcag agacattgat gcagcaactg 300
aagcaaagca caggcttgaa gaaagacaaa gagcagaagc ccgagaaagg aaggagaagg 360
aaattcagtg ggagacaagg ttatttcatt aagatggaga atgctgggtt tatgatgaac 420
cattactgaa acgtcttggg gctgccaagc attaggttgg aagatgcaaa gtttatacct 480
gatgatcagg gcagtaggca taattcagca acaaacaatc ttcctttggg agaaacctgt 540
tcattccaat cttctaatta cagtgggttc tatctcaggg atactggact ttctgacgca 600
gatgaacaat taaggggaaa agcttccctt ttccctctgt ggcagttacg attttgactt 660
cagtcctgag aaaaacttca ggttttgaaa atcagatgat gtcttctcct ttccaaaaca 720
ccacacgttg aaagcattta taaatccaag tctgaaactc tgcgctctag tactgctgtt 780
aagatacaca acttgtttct tagttcatat aatctcgggg acacacatac gtatacacac 840
acatacatat atataaatat acctgatgcc agattttttt cataaatatt ctgcctactg 900
taaatatggg ttctcttgag ttgttttaga aaattagcgc aatgtattaa aatcaagtgt 960
taggaaatct catggcttta cctacaataa cttttatttt ggaattgaac tattattaaa1020
ttgtatctaa tcctggaata cagtttaatt aattattctt agtgcttaag gcttcataaa1080
gtaatttttc caaccttttt tttaaaaaaa aaaaaa 1116

```

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 806 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
tccaagggct ctttagtcct tcctaagccc cacagtactt tcccgtagtc ctgaggcttg 60
ggacctcctg gggttcctac cttccctccc cattgctgag acagtctgag aagaggctta120
ggaatttgct tgtgggagtt tattcatctg tctctcctat ttacctctcc caaaccaggal80
tttccacttc tcaaacctgc tgtgatctca caactggagg gaggaagtga gctgggggggc240
tcactctccac tggctgcagg aacaggcctc cagggtctcc agactgatat tcagactgac300
aatgatttga caaaggaaat gtatgaagga aaagagaatg tatcatttga acttcaaaga360
gacttttccc aggaaacaga cttttcagaa gcctctcttc tagagaaaca acaggaagtc420
cactcagcag gaaatataaa gaaggagaag agcaacacca ttgatggaac agtgaaagat480
gagacaagcc ccgtggagga gtgttttttt agtcaaagtt caaactcata tcagtgtcat540
accatcactg gagagcagcc ctctgggtgt acaggattgg ggaaatccat cagctttgat600
acaaaactcg tgaagcatga aataattaat tctgaggaaa gacctttcaa atgtgaagaa660
ttagtagagc ctttaggtg tgactctcaa cttattcaac catcaagaga acaacactga720
ggaaaagcct tatcagtgtt cggagtgtgg caaagctttc agcattaatg agaaattaat780
ttggcatcag agacttcaca gtggggg 806
```

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 226 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```
gcggatocgg cgttctgcac tgatcttttc caagggtgta cagagatggc gccggggtttt 60
cggaaggcgg gtaagtcccg gcagcgggaa cacagagagc gaagccagtg actaccgtaa120
aaaacaagggt acctcaaagg tggtcgggaag aagggtgttg aaaaaaatcc agtgagttct180
actacaaaat gactcgggtt aaactccagg gtggggtaca aattat                226
```

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

"B3333" D3333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

gcagccgtcg ccttcggagc gaaggggtacc agcccggcag aagctcggag ctctcggggg 60
 atcgaggagg caggcccgcg ggcgcacggg cgagcggggc gggagccgga gcggcggagg 120
 agccggcagc agcggcgcgg cgggctccag gcgagggcgg cgacgctcct gaaaacttgc 180
 gcgcgcgctc gcgccactgc gcccgagcgg atgaagatgg tcgcgccttg gacgcgggtc 240
 tactccaaca gctgctgctt gtgctgccat gtccgcaccg gcaccatcct gctcggcgctc 300
 tggatatcga tcatcaatgc tgtggtactg ttgattttat tgagtgcctt ggctgatccg 360
 gatcagtata acttttcaag ttctgaactg ggaggtgact ttgagttcat ggatgatgcc 420
 aacatgtgca ttgccattgc gatttctctt ctcatgatcc tgatatgtgc tatggctact 480
 tacggagcgt acaagcaacg cgcagctgga tcatcccat cttctgttac cagatctttg 540
 actttgccct gaacatgttg gttgcaatca ctgtgcttat ttatccaaac tccattcagg 600
 aatacatagc gcaactgcct cctaattttc cctacagaga tgatgtcatg tcagtgaatc 660
 ctacctgttt ggtccttatt attctcttgt ttattagcat tatcttgact ttttaagggtt 720
 acttgattag ctgtgttttg aactgctacc gatacatcaa tggtaggaac tcctctgatg 780
 tcctgggtta tgttaccagc aatgacacta cgggtgctgt acccccgat gatgatgcca 840
 ctgtgaatgg tgctgccaaq gagccaccgc caccttacgt gtctgcctaa gccttcaagt 900
 gggcggaggg agggcagcag cttgactttg cagacatctg agcaatagtt ctgttatttc 960
 acttttgcca tgagcctctc tgagcttggt tgttgctgaa atgctacttt ttaaaattta 1020
 gatgttagat cgaaaactgt agttttcaac atatgctttg ctagaacact gtgatagatt 1080
 aactgtagaa ttcttctctg acgattgggg atataacggg cttcactaac cttccctagg 1140
 cattgaaact tcccccaaat ctgatggacc tagaagtctg cttttgtacc tgctggggcc 1200
 caaagttggg catttttctc tctgttccct ctcttttgaa aatgtaaaat aaaacaaaaa 1260
 atagacaact ttttcttcag ccattccagc atagagaaca aaaccttatg gaaacaggaa 1320
 tgtcaattgt gtaatcatg ttctaattag gtaaatagaa gtccttatgt atgtgttacal 1380
 agaatttccc ccacaacatc ctttatgact gaagttcaat gacagtttgt gtttgggtgg 1440
 aaaggatttt ctccatggcc tgaattaaga ccattagaaa gcaccaggcc gtgggagcag 1500
 tgaccatctg ctgactgttc ttgtggatct tgtgtccagg gacatggggg gacatgcctc 1560
 gtatgtgtta gaggggtggaa tggatgtgtt tggcgctgca tgggatctgg tgcccctctt 1620
 ctccctggatt cacatcccca cccagggccc gcttttacta agtgttctgc cctagattgg 1680
 ttcaaggagg tcatccaact gactttatca agtggaattg ggatatattt gatatacttc 1740
 tgccaaacaa catggaaaag ggttttcttt tccctgcaag ctacatccta ctgctttgaa 1800
 cttccaagta tgtctagtca ctttttaaaa tgtaaacatt ttcagaaaaa tgaggattgc 1860
 cttcccttga tgcgcttttt accttgacta cctgaattgc aagggttttt tatatattca 1920
 tatgttacaa agtcagcaac tctcctgttg gttcattatt gaatgtgctg taaattaagt 1980
 cgtttgcaat taaaacaagg tttgccaca tocaaaaaaa aaaaaaaaaa aaatgggtgg 2040
 cg 2042

"1992" 143255

(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2980 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

agcagagtta gccagaaatg cctcctgctg cccagcctt agagagctcc catctcaatc 60
 attgagcctg aaggcttcaa gcccaagaat gcaacaagac cccagccta catttctcag 120
 ctcccctgga gccagctgat cctgtaacgc tgctggaggt cagtctgagc taccaagact 180
 gtccctagac aaaggtggag tccccacac tgoccaagac caaatccctc actcaacctg 240
 ctgaggtgtg gatggggaaa cagaggcaaa actgaggcac ctgatgcatt cagcctgctg 300
 tgcagcagtg ccattgactg ccctgatgtt cagagagaaa cgcacacaag gtttgcccat 360
 gagaattggg gagcagatgg ccaagcagat aggttatgtc tgttttctga gtgatgaagt 420
 caggaagccc tgtggctctg gaggccactt gtggttcatt cttttcccat atccttggtc 480
 tttagaaatg gttaccttca ggacagtga cctgcattda tcagagcact attgctaagt 540
 tttcttttct ggcttgtgtt tttctgggac agtttagaat tgggaggcct attctcatag 600
 aacacaaaaa atgatgttca gtgattcatt taacatacac caatgtactc tggctgctgg 660
 ggggacaacc ataagcaaga catgcccagg gtttgccgtg gctccagatc tactccctgt 720
 aggagtcca ggatcacaca aacggtagta accagggttg tgaatctgag tacacctgg 780
 caaggcttct cttcagactg aagcagcaat cctgccacta ccagcagcaa ccaggacgtc 840
 tgttctttgt gggggccaga tcagaagaga gagggccctg tgacgcccgg gctgcttggt 900
 cacaactctg tccaattcaa ggatgtttat cggcctctct tagatcctga gtgagacaaa 960
 tacagaaatg acccattccc tgcccaccag aaactcagag gtgattgggg agactgacac 1020
 aggaaaaatga acttaataca gagagactgt gatattgtct aagaagggtg tgagggaggg 1080
 agagatgaat tttccctgga gggatcctag aaagcattgt catattgcca tctccattag 1140
 ctactttta aacaactagg gtgctggaag aacctttgtc tgagggtagt tcatagctgg 1200
 aaataacttg aataatttcc agagtctcta aactctcatc ttccccaca gatacacatc 1260
 caagctcaca aataggagta gcaattctag gtggtagggt tgtgtacgga acccctgggt 1320

 gtctgcatat atctcagaat taccacagga ccattgtccc aaagtctaga gtctttacag 1380
 gtaggcaaaa tttgttttca atgctgtgct ctcagctgct gtcacaaaata cccatcttag 1440
 gatcccatca gcttcccatc ccccaccaga cagccacagt accctcactt tctccctatt 1500
 gttctttcaa atcctgttct caggaaagaa actgccacta attcattcac actaagggtg 1560
 aaatgattga taataggaat gagttacctc ttcccacaga catttgtttt taagtatgac 1620
 agagcagggc cttaatccca agggaaaagg ttatggaact ggaggggggt agctttctgg 1680
 gtagaaggag acttccctgaa tttccttaaa acccagtaag agtaagacct gttgttttgg 1740
 aaggctctgt ccaccatcta agagcactgt tttttttttt gttgttgttg ttgttacggt 1800
 ctctgaggga atatagtaaa aatgcatatg cacgtgcaat ttgcacggca gcatttcacc 1860
 gattgtggac tgtattggct aatgtgtttc ctggtcttta gatgcaaac attaatcaac 1920
 ctatcttatc toatagtttt ttcagggtgt cttcttgatt agtagggaat tttgaacacc 1980
 tctttaaaata cagctagaaa ataaaaacca tttgtaaagc cacatttgca tatgatgcca 2040
 gcctcacgca ttgtatatc tccagaaatt caggatagcc tcaccaattt gccctctttt 2100
 aataaaatct tgtgttaaaa tttgcatcac gtgccttcc tatgtatgac gaaacaagaa 2160
 acagagattt ccaattgctc ttttgtcttc agacatttag taatataaag tacctatttt 2220
 tatgctgaaa tgtttatata ggtttattaa tagcaagtgc aactaactgg cggcatgcct 2280
 tgcaacacat tttgatatat tagccatgct tccgggtaaa ggcaagcccc aaactcctta 2340
 tcttttgag tctctctggg atcagtaaaa gaaaaaaaaa ataatgtgct taagaagtgg 2400
 gactgtaaat atgtatatat aactttgtat agcccatgta cctaccttgt atagaaaaat 2460
 aattttaaaa atttgaatgg aagggggtaa agggagtcac gaagtttttt tgcattttta 2520
 tttaaatgaa ggaattccaa ataactcacc tacagatttt tagcacaaaa atagccattg 2580
 taaagtgtta aaatttacga taagtattct attggggagg aaaggtaact ctgatctcag 2640
 ttacagtttt ttttcccttt ttaatttcat tattttgggt ttttggtttt tgcagtccca 2700
 tttatctgca gtctgattaa gtctatttgc tagaataggt tactacaaaa aaggttatat 2760
 tctgaaagaa aaataactga cattatatat aaccaattaa tttaaagtat tgccatttta 2820
 attacacact gagagcatgt cctatgcaga catagatttt tctgttcatt tattttcttt 2880
 cattgcagtg gattgatttg ataaatagat gtgttgaatt actacatttg ctgtacatat 2940
 tatttaataa actttattca gaattgcgtg gcaaaaaaaaa 2980

35573540 "076544"

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 227 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

cagcattgct ccacggcaca gcataaggat agatcccaag tccacagggt ccattttgca 60
ggtcattatc tgatccctagg aaatgtcctt ttcccatagt tgctctatgc ctttgggggtt120
tagtcctatcc caggggtaac tgtggagaaa tcattgggtt gagagtcaag agagcattgg180
ttttggagct ttaatccctt tctggttgaa ataagggtgt caacttg      227

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(2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 773 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

cggaagtgtgta aagggttctgt cctctctctgc gccaggcgga acctctctgc tgggcccgggt 60
ggcgcgcaaaa gaactttctt tctcccgcgc gaacggctgc cgcgccaac tgcctcgccc120
gcctggcagc ctaaccctcc ttctctctt ctcctctccg gcttcgcgcg gccctgcctc180
cctctcgccc ggcgccatcc gcttgctgct gccaccgcct cctcatcttc tgcggcgcca240
acgggctgtc cccgctgcag tgatgtgcga caaggagttc atgtgggccc tgaaaaacgg300
agacttgat gaggtgaaa actatgtggc caaggagaa gatgtcaacc ggacactaga360
aggtggaagg aaacctcttc attatgcagc agattgtggg cagcttgaaa tcctggaatt420
tctgctgctg aaaggagcag atattaatgc tccagataaa catcatatta ctcctcttct480
gtctgctgtc tatgaggggc atgtttctgt tgtgaaattg cttctgtcaa aggggtgctga540
taagactgtg aaaggcccag atggactgac cgcctttgaa gccactgaca accaggcaat600
caaagctctt ctccagtgt ggatggatgg actgataact ccggaagaat gactctcctg660
tggcctcaca ctgctgctg tctgtctgtc actctctatc tgccagcttc ttcagctaaa720
tactttaaga ggggtgaggg gagagagaaa ttcataacaa atccgactac cag 773

```

(2) INFORMATION ON SEQ ID NO. 77:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

gacccggcgt ggctactagg agaaggacgt acggtcctgc tagtagagga atatgtcgag 60
tttctctagg gcgccccagc aatgggccac ttttgctaga atatggtatc tottagatgg120
gaaaatgcag ccacctggca aacttgctgc tatggcatct ataagacttc agggattaca180
taaacctgtg taccatgcac tgagtgactg tggggatcat gttgttataa tgaacacaag240
acacattgca ttttctggaa acaaattgga acaaaaagta tactcttcgc atactggcta300
cccagggtgga ttagacaag taacagctgc tcagcttcac ctgagggatc cagtggcaat360
tgtaaaacta gctatttatg gcatgctgcc aaaaaacctt cacagaagaa caatgatgga420
aaggttgcat ctttttccag atgagtatat tccagaagat attcttaaga atttagtaga480
ggagcttcc caaccacgaa aaatacctaa acgtctagat gagtacacac aagaagaaat540
agacgccttc ccaagattgt ggactccacc tgaagattat cggctataag agaataagaa600
ttgcagaaaa taacagtga gtgattgaaa ctttcttctg atgagtttct ctaacctaca660
ggatggagta aaacaactgc tacagttcag cactgtttt atgtgcccga tcaactgtgg720
gaaaggtcag gaaggtgtag tccctcaata ggaaattgta attaaaatat aattttatag780
aaccattttt atgtaatctg atttgaatgt tatagttgat aataataaaa tcacttactt840
ggttgactaa aaaaaaaaaa aaagtcgacg 870

```

(2) INFORMATION ON SEQ ID NO. 78:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ttgtgatcgg ctatcccttc cggatcaaca gcgagcccag cccggtcatc tacaaccggc 60
ccgggaacaa cgtgaaactg aactgcatgg ctatggggat ttccaaagct gacatcacgt120

gggagttaac ggataagtcg catctgaagg caggggttca ggctcgtctg tatggaaacal80
gatttcttca accccaggga tcaatgaccc attcagcatg ccacaaagag ggggtggc 237

(2) INFORMATION ON SEQ ID NO. 79:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 439 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

"04922950" 05673644 030504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

gtttgggaag ttgagatttg gagcgaataa gtagggatct ggcaagagga tcattctacct 60
cagtcattag gatttcttaa taaaaaagag attgtatttt tgagttggtt attaaagatta120
ttaaaattag cccttccttt gaaatatgac atcagctttg ctgttctaaa tttaaaattal180
gttgcttcat cagtagcaca cttccagttt ctataccaag ccagtccttct cagttttccc240
cttaggatgg gacaagtctg ttcagggggg cattctgtaa ggttcagcag ggggtttggg300
agaggattta aggggaaata cagtgggggc agaattgggtt cgggggtaaa ggtaggggac360
aaggaggagg gggcgaaagg aggggtggaa ggatgggggc cttacctaga tcgggggatg420
ccgggggggc aaggcaagg                                     439

```

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2483 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

"GSE" FILE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

gcaaaagtct tcaaactatt gagaaagagc catagactga gtgcaggcac cagtgcgctc 60
ttattactgt gtcaattaaa tgaatgtatt tgaatgtttg gatacttacc tctgaatgta 120
ttttgagtaa taacttcaag tgcaattat gccatgcata atttcttttg tctcatgttt 180
ttccccctt ttcttttagg ctttgtcttc tgagtctata gaaaaacttc cagtttttaa 240
caagtcagcc ttcaaacatt atcagatgag ctctgaggct gatgactggg gtatcccaag 300
cagggaaacca aagaacctgg caaaagaagt ggccatgtga agagggacac tcaggacact 360
ttacgggagc aaagtgggtc tacaccagtg ctgcttcctg aatgtttgtg tgtgaacctt 420
tgtttcctcc aaaacaaacg acagcaacga aaactcctta atcagaacac tgatccaatg 480
aggaatggag cttgtttctg tgacccagga gaacttagtg caagactaca ggagttaaca 540
gatggccagc tccttatttt ttaatgtaga ataactcctg agtttatatc aaactcctgaa 600
gaaataagcc tcagttttcc atctgttttt gataagaata agaaagggag tgagtgtgaa 660
gatgggtggt agcagtttca ctaagactga tatttttagg ctcttggttca catcaaaaga 720
tattggtgtc agaataccag cattttcctg ccatgcaaag gattaaaact tagtttacac 780
tatgtggtta caaatatatg tcaatgtaca ttttgaacat atttatgtgc tatggaagga 840
aatgctggtg actaaaataa ggtttactct gaaagaggag gaattttatc caaagcattc 900
aaacatttta ttcaagtgtt tcaaaattca aagcattgta ttcaaagttg cagtgaaggc 960
atcaacttat gtaaaaaactc agaaggaagg ctctctctgat aaaaacacag ctcttttatt 1020
atgctgcttt tcttgttcac ttacacact aagtaaacac ttattgtcag gtgcctagtc 1080
ttgagtgaat tgrtagatgt gcactgaact cgggatgttg gggattggag agagagaatt 1140
gccaaagtaa cagcaaaaaa atctcttact ttgctttggt tataaataaa ttagtagatt 1200
ggaaaaacta gtgttaggga aagaaatcac atgttcagag cctaattcag taggaagggc 1260
ttttctctac cctgaaatga aggtaatcca aaggcatcca ttttctaggc ttaaaagata 1320
tatttttgat atatttaatg atattctcta cactccagca ttaatatgtc tgtttaaaaa 1380
ttactaatc tcaaatggct caagaacatt agaatttaag taccttttag agtaattatt 1440
ttaagcaaat agcctggacg taagagattc tcatgccagc atgctttcat ttgtcagttg 1500
ttgtgactga gagataatga atgacacctg aaatgcata ggtatttttg ggagagttaa 1560
ggtataatct gaagggttgg agaccagttg ggctgattac tcttagagaa gaagaaatgg 1620
aaaaatgaaa gaaggcagga aggaaagaaa ggatatagga agagagggaa gcagaaggca 1680
ggcatttttc tattttcccc acaaattatt tcaaaaaaaa tctgtatttt ctgggatatt 1740
tcattggcaa gaggaagaac tgggtgtttg aaagcagtat ggattcttta aatgcctctc 1800
actcttacaa gatagtaggc tttgagataa taaacttacc cgtgtcaatt aacattttaa 1860
ctggcatata gaaaaaaagg aggatttttc tgcattgtaa aataatcagt atgggtttata 1920
tgttgaatct gacatttgtg tgtaatttca tgggtggccta gtgttgtggt gcttctggta 1980
atggtaatat aagctcaact atttttttgt ggatttcagt ttttatcatc agaagtccta 2040
gacagtgaca tttcttaatg gtgggagtc agctcatgca tttctgatta taaaaacag 2100
tttgacagtag gttatttgtc atttcagttt tttactgaaa ttgagctaa acatttttac 2160
atgtaaatat ttgtatttac caaagattta aatcagttga ttaattaatt aactcaaata 2220
ctgtgaacta tctttaaaaa actagaaaaa agaaatgtta gtatctcaat tacaccaact 2280
gtgcaaatga actttgataa aatagaaata atctacattg gcctttgtga aatctgggga 2340
agagcttttag gattctagta gatggatact gaatactcag gccacttaa tttattaatg 2400
tatacattgt gtttttgtct ttatgctatg tacagagaaa tgtgataatt ttttataata 2460
aatatttttt atgatgataa aag 2483

(2) INFORMATION ON SEQ ID NO. 82:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 353 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

ggtggtgggg ggggggggtgt tgggccaaaa gacttcggta tctgacaaca gcatcatcta 60
cctcagtcac tagggtttct taataaaaaa gaggttgta ttttgacttg gttattaagg120
ttattaaaaat tagcccttcc ttgaaatat gacatcagct ttgctgttct aaatttaaaa180
ttagttgctt catcagtacc acacttcag tttctatacc aagccagtct cctcagtttt240
cccattagaa tggacatgtg ctgttcagcg tgtcatgtct gtaatgcttc atgcagagag300
tttggtcata gtattaaaga gaaaatacag tgaggtcaca atgtctccag agc      353

```

(2) INFORMATION ON SEQ ID NO. 83:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

cgggggataac caaacacagc tgtttacggt ttctccctta acccatgctt tcataaacc 60
cttcggacag cttccccgct caggctttct aaccacacct accccagggg tgccgcattc 120
ctgcactcag aagtctgcag cggtcctca aaaaacttga ttgtgccata aaaatcactg 180
gggatcttgt taatacagct tctaactcaa tagatctggg agatcctgca tttctaacaa 240
gctcccaggt aaggcggagg ctgctggtgt gaggaccatg ctgtgagcag cagggcgaga 300

gtgcccaggg ctgatatata ttggaaatat cacccttgaa gccatcgctg gccccacact 360
cctgtggact gatgccccag ggattcccac cccacttctg caaccccagg tatccttcat 420
tatccacccc atcccagact cccaccccag ggattgcccg tgaagacttt ggcttagcaa 480
attgtgttgg ttatgtgagt gttgttttaa tcagagatgt acatgattgc caatctgcat 540
ttcttaccag tgtgaccaca ctgttacgat gcaattctag ccaaaaaaaaa actttttcct 600
agtcttatgg aaagcaaata tacaatgatt ttcagtaggc ttctggaata gaaacagtgg 660
tttgaagacc ccactgccac ctttatggac tggccccttt gagtctgaat ccccgccctc 720
tgtcacctga gacccaaccc ctgactgggc caactccagt gaattcacc atttttcttc 780
ttcagaaggc ctttctgtg tgagaccac atattttaac cttttgctcc tatcccattt 840
ttaaagaatt agagaataaa ccaggcctgt ttcttttccc ctgaaatccc tgctctggc 900
ttcctaaacc catcatctaa ggtgacagag cagtgtctgg aataggcatc ttcttttcaa 960
ctttcccaa actggccaca gataggctgg ccatgggaag ggtcttttga tttcggggga 1020
ggcaaactg ggggattgt
1039

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(2) INFORMATION ON SEQ ID NO. 85:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

agtgtatttca gcaaattgagg gtcagaactt tcagtttatt gatgggttatt cagccgcaga 60
tgagagtttta tgcgtcagcc acttcaattt ctgtaaacag aggcacaggc caaggactgt120
aaggggcaga actagttttt cttcaaaatt gcctaggcat aataaggaaa atagcacttt180
tatttcaagg aaaccgatgg aatgttcaaa tgaggaagtt gttaatcaag ggcagtcgga240
tggtatcaatg ggtaaatttt aggtggcgtc aaggaggggc ttatattcac tcaaaccgg300
atgttattttg gtcgggccaa ggttgggaagg

```

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 235 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

atttaagtat tttttagttt ttaaaatgtc tttccggtga gggaaggagc cccagccaga 60
aagcaattca atcatgggtca agtttccaac tgagtcattt tgtgagtggg taatcaggaal20
aaatgaggat ccaaaagaca aaaatcaaag acagatgggg tctgtgactg gatctttatcl80
atccattcta aatccgattg aatattgcgg gttacaaaa tgccaagggg gtgac 235

```

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

caggaccagc ctggccaaca tggcaaaacc ctgtctctac taaaaagtaa aaaaaattag 60
ccgggcatgg tggccttgtc ttgtagtccc acttcagtct aagtagctgg gactacaggc120
acgtgccaca agcccagcta atgtgggtgt tttgttagag atgaggtagg gccatattgc180
ccaggctcgt cttgaacacc ggggctcaag gaatctgccc atcttcgcct cccaaagttc240
tgagatagca ggtgtgagtc atcatgccca gcctccttga agtttactaa caattgggat300
aactgagggg agagaagtga caattccact cagtctatta gaggtctgga tataaggtag360
ccacacaata actctaactt gacttctaac cattctatct tattgatttg gaggctgtct420
tctgccagat tttttgtggc ttgagatgat attttcgaac ccttctttca ctacctttct480
tacccttaat gtgccaaagc tgaaacagga tttgatttcc tgagctactt gttcgccttc540

tgtgcgtcac caagtaatct ggttcattct tcgtctcatt catgttattt tcaagtga600
caagacattt tgggggtcaa gtctcttttg gtgttttgtt tttatgtata taaaaatgga660
ttttgtgttc cttttccatg taagtaccaa cttatatgga aactcacaat cataatgtaa720
agaagaaatg aaagcctggt gtattgtact tcaagatgcc tccctgatgt atagaatctc780
cttgtaaaat aaataattgc attgtatata agtcttccca tcaatattaa ttattaaata840
ttttagaatt tttaaatacc aactat                                     866

```

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 846 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctccttgtcc aacggaaaaa acatggaagg gttaagccta aacaaccctc aaacggaact 60
ttatgccaga aaacaactac ggaataaaaaa cccacaaaaa tacagagagg aacgttttta120
accttttaggg cctgcgtcct ctgcctttgg cccatcaggg tcaaagagta ggagtgagga180
aggaagggat gggacagcat cccctgggac gttcaagtac catccctggg ctccactctc240
cagccttaga gagtggacca gccagagcac ctgctctgga ctctcagacc tgctgctttg300
tctctaccaa ccttggcagg gatctaggat ccatttagtg ggatcaggtc ccagtcaata360
ccattggggc tcaaataagt tcttagaacc acagagtcta gggccagggt cccaactcat420
aggtgacgga gttccctttc aagctcgtgc cgaattcggc acgagcgggc acgagcttga480
agggaaactcc gtcagctatg agttgggacc ctggccctag actctgtggg tctaagaact540
tatttgagcc ccaatgggat tgactgggac ctgatccac taaatggatc ctagatccct600
gccaaagggtg gtagagacaa agcagcaggt ctgagagtc agacgagggt ctctggctgg660
tccactctct aaggctggag aaggagagacc aggatggtac ttgaacgtcc cagggatgct720
gtcccacccc ttccctctc actcctactc tttagacctg atggccaaag ccagagacgc780
aggccctaaa ggtaaaaacg tctctctgtg attctctggc ttttactccc tagtgtctct840
gcataa

```

846

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cgaaagcgctc ggactaccgt tggtttccgc aacttcctgg attatcctcg ccaaggactt 60
tgcaatatat ttttccgcct tttctggaag gatttcgctg cttcccgaag gtcttggacg 120
agcgctctag ctctgtggga aggttttggg ctctctggct cggattttgc aatttctccc 180
tggggactgc cgtggagccg catccactgt ggattataat tgcaacatga cgctggaaga 240
gctcgtggcg tgcgacaacg cggcgagaa gatgcagacg gtgaccgccg cgggtggagga 300
gcttttgggtg gccgctcagc gccaggatcg cctcacagtg ggggtgtacg agtcggccaa 360
gttgatgaat gtggaccag acagcgtggt cctctgcctc ttggccattg acgaggagga 420
ggaggatgac atcgccctgc aaatccactt cacgctcatc cagtcccttct gctgtgacaa 480
cgacatcaac atcgtgcggg tgcgggcat gcagcgctg gcgcagctcc tgggagagcc 540
ggccgagacc cagggcacca ccgaggcccg agacctgcat tgtctcctgg tcacgaacc 600
tcacacggac gcctggaaga gccacggctt ggtggagggt gccagctact gcgaagaaag 660
ccggggcaac aaccagtggg tcccctacat ctctcttcag gaacgctgag gcccttccca 720
gcagcagaat ctgttgagtt gctgccacaa acaaaaaata caataaatat ttgaaccccc 780
tccccccag cacaaccccc ccaaaacaac ccaaccacg aggacctcg ggggcagagt 840
cgttggagac tgaagaggaa gaggaggagg agaaggggag tgagcggccg caccagggc 900
agagatccag gagctggcg ccgccgatca gatggagaag gggggaccca ggccagcagg 960
agacaggacc cccgaagctg aggccttggg atggagcaga agccggagtg gcggggcacg 1020
ctgccgcctt ccccatcacg gaggtccag actgtccact cgggggtgga gtgagactga 1080
ctgcaagccc caccctcctt gagactggag ctggcgctctg catacgagag acttggttga 1140
acttggttg tcttgtctg caccctcgac aagaccacac tttgggactt gggagctggg 1200
gctgaagttg ctctgtacct atgaactccc agtttgcgaa ttatagagac aatctatatt 1260
gttacttgca cttgttattc gaaccactga gagcgagatg ggaagcatag atatctatat 1320
ttttatttct actatgaggg ccttgtaata aatttctaaa gcctctgaaa aaaa 1374

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 761 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

gcctgatggg ctggagccag actgtggtct gaggaggaga cacagcctta taagctgagg 60
gagtggagag gcccggggcc aggaaagcag agacagacaa agcgtagga gaagaagaga120
ggcagggaag acaagccagg cacgatggcc accttcccac cagcaaccag cgtccccccag180
cagccccccag gcccggagga cgaggactcc agcctggatg aatctgacct ctatagcctg240
gcccattcct acctcggagg tggaggccgg aaagggtcgca ccaagagaga agctgctgcc300
aacaccaacc gccccagccc tggcgggcac gagaggaaac tggtgacca gctgcagaat360
tcagagagga agaagcgagg ggcacggcgc tgagacagag ctggagatga ggccagacca420
tggacactac acccagcaat agagacggga ctgcggagga aggaggaccc aggacaggat480
ccaggccggc ttgccacacc cccaccccct aggacttatt cccgctgact gagtctctga540
ggggctacca ggaaagcgcc tccaacccta gcaaaaagtgc aagatgggga gtgagaggct600
gggaatggag ggcagagcca ggaagatccc ccagaaaaga aagctacaga agaaactggg660
gctcctccag ggtggcagca acaataaata gacacgcacg gcagcacaaa aaaaaaaaaa720
aaaaaaaaatcc ttgttaaaaa aaaaaaaaaa aaaaaaaaaa a

```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1825 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

aggggaagcta gtagcggacc ggaagtgagg caccctcggg ctcgagacag cggcgacggt 60
taaagctgag cgacccagtg ccactggaga cggtcagctt ctccactcag gctcctccag 120
cccgagccag aagacccctt ccccagaaat tctggggggc gatggaagg agccgagtca 180
gatcgcgagg taccagagc cgacagaccg gagcgacagg gagttgccag aagccccgcc 240
cctaggagtg atcggaagc ctcacccatc cgggtgagga acccgagga ccgcctccgg 300

gcgagagcgcc gaccatggct acgcccctgg tggcggttcc cgcagctcta cgcttcgccc 360
ccgcggttag ctggcagggt gtgcgaggac gctgcgtgga acattttccg cgagtactgg 420
agtttctgag atctctgcgc gctgttgccc ctggcttggt tcgctaccgg caccacgaac 480
gcctttgtat gggcctaaag gccaaagggt tgggtgagct gatcctgcag ggccggcctt 540
gggcccaggt cctgaaagcc ctgaatcacc actttccaga atctggacct atagtgcggg 600
atcccaaggc taaaaagcag gatctgagga agattttgga ggcacaggaa actttttacc 660
agcaggtgaa gcagctgtca gaggtcctct tggatttggt ctcgaagctg caggaaacttg 720
aacaagagta tggggaaccc tttctggctg ccattgaaaa gctgcttttt gagtactttg 780
gtcagctgga gaaagcactg cctacaccgc aggcacagca gcttcaggat gtgctgagtt 840
ggatgcagcc tggagtctct atcacctctt ctcttgctg gagacaatat ggtgtggaca 900
tgggggtggct gcttccagag tgctctgtta ctgactcagt gaacctggct gagcccatgg 960
aacagaatcc tctcagcaa caaagactag cactccacaa tcccctgcc aagccaagc1020
ctggcacaca tcttctcag ggaccatctt caaggacgca cccagaacct ctagctggcc1080
gacacttcaa tctggccctt ctaggccgac gaagagttca gtcccaatgg gcctccacta1140
ggggaggcca taaggagcgc cccacagtca tgctgtttcc ctttaggaat ctgggctcac1200
caaccaggt catatctaag cctgagagca aggaagaaca tgcgatatac acagcagacc1260
tagccatggg cacaagagca gcctccactg ggaagtctaa ggtccatgc cagaccctgg1320
ggggaagggc tctgaaggag aaccagttg acttgccctg cacagagcaa aaggagaatt1380
gcttggtatt ctacatggac ccctgagac tatcattatt acctcctagg gccaggaagc1440
cagtgtgtcc tccgtctctg tgcagctccg tcattaccat aggggacttg gtttttagact1500
ctgatgagga agaaaatggc cagggggaag gaaaggaatc tctggaaaac tatcagaaga1560
caaagtttga caccttgata cccactctct gtgaatacct accccttctt ggccacggtg1620
ccatacctgt ttcttctctg gactgtagag acagttctag acctttgtga tagaactaaa1680
atgctctctg tactctagtc tctgcctcc tcagctctgc aagtagttta gtaggaatga1740
agtgggaagtc caggcttgga ttgcctaact acactgctaa aaatatttgt aatccttaaat1800
aattaaactt tggatttgct aaaaaa

```

1825

"000000" 000000

(2) INFORMATION ON SEQ ID NO. 95:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

ccgggattcg ccctccgggg agcgattggt cctcggggagg ggcggggagg tggacgcggg 60
taccggcggt cgtcggggtcg gcagcctttg gtcagttggc agcggcaagc gcgctgcggg 120
tccggtggcg ccatgtcggt ctgcagcttc ttcggggggcg aggttttcca gaatcacttt 180
gaacctggcg tttaactgtg tgccaagtgt ggctatgagc tgttctccag ccgctcgaag 240
tatgcacact cgtctccatg gccggcggtc accgagacca ttcacgccga cagcgtggcc 300
aagcgtccgg agcacaatag atctgaagcc ttgaaggtgt cctgtggcaa gtgtggcaat 360

gggttggggc acgagttcct gaacgacggc cccaagccgg ggcagtcccg attctgaata 420
ttcagcagct cgtgaagtt tgtccctaaa ggcaaagaaa cttctgcctc ccagggtcac 480
taggcgggca gcccacaccc accccagacg gccaccacac tgaggccaca cgttggccat 540
tccaccttgg agttggaacc ctgggcgtcg agacaggaag gcagggcgca gtggttgaia 600
catcaggaca ctcccaaggc cccggctctg aacaagacct ttctgtttct tggaaaagag 660
actcatttgc tgatggttca tgccttctgc tgggacaggc ctgggctgtg cagccacact 720
gtcggctgac ttagcccccct gctcactcta ggtgcctcca ggaggtgagc cctgggtgca 780
gctggtctct gaatgacgtt acacccctcac cttcttttcc tggccctgtc tctggactct 840
cccctgtgag gcccaattcc aagacagact ctctcctca ccgaagctta ggcccacatc 900
tcccaggctg cttaggagac agaattgaaa cggaggccgc ccctgccagc cgccctggcc 960
ctggtcactg catgatccgc tctggtcaaa cccttccagg ccagccagag tggggatggt1020
ctgtgacctg ctgggaaggc aggtgatgg gccacaccct tggcctctcg tccacgaggg1080
gagaaacctt aacctgttt cacaatctgt gcggaagtag cttgcctcac ttctgcttag1140
gaaagcggct gttgctccat aactctaacc agcacagggc tgaggcctgc agtgcacacc1200
tgcagggagg cccttcccaa ggtgtggtga ctgtgcctta ctgtacatgc tccgaggcct1260
ggccatatag gaggggtgggt gatgctgaaa tcacccccca tcttaagtaa ttactttctg1320
gagtaatcag gtggaaatcc atagacaaat gaaacattca gatgtaaaaa aaaa 1374

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2615 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

cttgggaagc tcctggatct ttgtcaacct gactgtgcga ttctgtatct tgggaaaaga 60
gtccttttat gacacattcc atactgtggc tgacatgatg tatttctgcc agatgctggc 120
agttgtggaa actatcaatg cagcaattgg agtcactacg tcaccgggtgc tgccttctct 180
gatccagctt cttggaagaa attttatttt gtttatcatc tttggcacca tgggaagaaat 240
gcagaacaaa gctgtggttt tctttgtgtt ttatttgttg agtgcaattg aaattttcag 300
gtactctttc tacatgctga cgtgcattga catggattgg aagggtgctca catggcttcg 360
ttacactctg tggattccct tatatccact gggatgtttg gcggaagctg tctcagtgat 420
tcagtcattt ccaatattca atgagaccgg acgattcagt ttcacattgc catatccagt 480
gaaaatcaaa gtttagatttt ctttttttct tcagatttat cttataatga tatttttagg 540
tttatacata aattttctgc acctttataa acagcgaga cgccgctatg gacaaaaaaa 600
gaaaaagatc cactaaaaag aaagatttag atggcttctt gccagtttga gcctaattctg 660
attcttcacg ttttaccttc ttgaaccaat gtaaaagtgt ttttaagtgt aaatgattaa 720
attctcagtg aggtatcttt ctttttcccc agtaacattc ctgaatttac tgttatctta 780
ttgtagtact tgcattgacat ggattcctga tatctgatga gaggttcatt cttgtgtatt 840
cagttaatga caccaaaagg ctacagccac cccaacccta tctcatgttc agtctgtcta 900
atacatgcca gagatttttt tttcaaaaag tgctttatcc ctacaatgta ctgacagttc 960
ttacagttga gatttgttct tttcagctat tgcttgtgaa aaaaagcaag actatgtcac 1020
tctatagaag gctgttaaag tgactcaggg aggaattaat tattctgtac ctaaggggtt 1080
acttgtttta tgggatggca ttgacttttt gaaaatcaag tggactgagt cattgataaa 1140
acatttctaa gagtggggct agagaacata ctttacatct gacatccttt ggcctaacaal 1200
catctattat tatagtgtc agcagtgtgg gcatggaaga ggccgcagaat gctttgaaag 1260
aaactaatca gaatcttggg acatcatgat catgccattc ttaagttaat caactatttt 1320
caacactgaa gaaaaatgaa acattattta gaaaacaatg agattacaag ttccaaactc 1380
agccaggaat gtggctcaca cctgtaatcc cagcactttg ggacacctag gtgggagcat 1440
cgcttgaagc caggagtcca agaccagctt gggcaacgta gtggagaccc ctatctctac 1500
aaaaataaaa aaaattagct ggggtgtgatg gcacacacct gtttgtccca gctactcaag 1560
aagctgagat gggaggatcc tgagctcagg aggtcaaggc tgcaagtgagc cgagattgtg 1620
ccactgcact gcagcctggg gtgacagtgc aagaccctgt ctcaaaccac accaaaccac 1680
acacacacaa acacacatac acacacacac acacgaggtc caaatggtag cagggatcca 1740
aagggaacac agtatgtagg tcaaactggc agtaacagtg tacagccttt gacaaactag 1800
aaatattaga gtaggccaaa cacacctcca aactgttaagg ctgtgcacaa acataaaaaa 1860
tggcagcctt ccatctcctg cactggctga gtccatttac ttgtgtactt gttctagtga 1920
gtgggtgggac tgtacatttt tgaatagacc tcaaaaatac ttcattctgc tgctgttcag 1980
ttggcttttt aaacctgtct gcagtaggac actgaaaaca gcaagaactt cgggggtgaa 2040
accgctgat cctttaacaa ggatttctgg caggaaactc acaaaaagga gaactgaaaa 2100
tttagacata cagttggcca ttgtaaaaaa catcagtttc ctctcataca ttccaagtaa 2160
accaagtaaa ataagtgttg gagtaacact tgcataaaaag aatttaagga gtgatagctc 2220
tttctgttct gccattccca acattcctgg gggaaaggag actcaatgag ttaatactat 2280
ttcactgagc ccaagatgga aacttggttt gacctaaaac atctgattaa tataggctag 2340
ctgatttctt aaaaattcgt tgcattgaag gatattttgc atgtctgtaa cacctgtcaa 2400
tacttgtttg tattgatttc tgatattcct gcagctgact acgtgttaatt gggcagatca 2460
gctttgcagt agattatgct gcatcctcgt ggcaaaaattc tgtattctta gtgattgtta 2520
caaaccctt tattgctgtc tgagaaaagt aaagattgtg tatttctatt aaaacattta 2580
caatcaaaaa aaaaagaaag aatagaagaa aaaggg

```

2615

(2) INFORMATION ON SEQ ID NO. 97:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 508 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

gttggcagaa acccggtatc cggttccggt gggcctccat cagcaagctc cagtgcctacg 60
tgtccctggc attttaggtg tcggttggtt aggcagtcac ggatcaggta atgcagtttg120

ttgagccaag tcggcagttt gtaaaggact ccattcggct gggtaaaaga tgcactaaac180
ctgatagaaa agaattccag aagattgcca tggcaacagc aataggattt gctataatgg240
gattcattgg cttctttgtg aaattgatcc atattcctat taataacatc attgttggtg300
gctgaataca ttttggaaga gagtttttca tcttagagat tgggtgaaca gtgtgagggg360
gtgagaaaact cacagaatac aaatttgcct gtatgttttg tgggtttttt tttttccttt420
caagatgttt tctatttcta aattaaagta atttcaaagt aaaaaaaaaa aaaaagtcga480
cgcggccgcg aatttagtag tagtaggc                                     508

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(2) INFORMATION ON SEQ ID NO. 98:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3588 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

ctccgtotca aaaaaaaaaa aaaaaaaaaa aaaaggggaag ggaatcccat tttgtgatga 60
tttgggcaca ctacttgagc tgaggctagc agtcacatga ttttggctgt ctctgacctg 120
aagcttttga agtaagggtta tgtctcttcc ctgaagcttt gtttatagtg gtaatttggg 180
gagtttgagc tttgagcttg tcttagaaaa taagactgtc cacctgggga ggggagctta 240
taggggaacc gtgttaactc agaagtgctg agaaagtgtc tttagccaac aaaagtaaga 300
ttactatcta gaagggtgaa agaagtcatt gcttctgttc ctccagcagt cagttgactc 360
taggtttcct ttggtttata tccccagttc ttaatactaa aacttatttg acttctatc 420
aggaagcaca caaaaaaagc gtcattttaa accctggata taggctttaa aggatacaaa 480
aacagcagca ttgtcggttt gccagggttc tcaccatttt gatgtgctac ccctccttcc 540
accctccctt tctgcccccc aagcctccca gccaggccag atgtgaagat tctattaatc 600
actgtttcag agaacattaa ttcttgata gaataattat ctactaaatt gcttattatc 660
tgtgactacc ttgcagagaa catctcaaca gtgcagtaaa atagctctcc tagacttgag 720
cttcagcca ggcatttga tcaactttaa gcctttgtgg aattctgagg aaaaaagca 780
agatgcctca atgccaatgc tgggccataa gattctactc cctcctgt aggggtgggc 840
gcgtggctca gctttgaaa atcattttgc cagtaatatt gcctgtgaat ccctttaaga 900
agtgcctcg atctgagcct gtctttctga gcactttgg gctgaattga aaatggtaag 960
ctaaagcagt gacagatcca cgtagcctct ttaacctctt tattatcttg ccaaaaaaaa 1020
agtttctcag gttaaaccct tgtctttaac ctccctttgt tgtggagaaa atgtgtcact 1080
aatcagtggt ccaagggata tctagctttg gttactcagt tctgcagca taacagatat 1140
gacttatgcc aggggaagga gaggtgatt atggagacac ccaggaacag gaataagaag 1200
ggataggtct gtcacagta gaacctcccc agatcggaag ttaagtcttg gagagtttcc 1260
aaagtgtcga agtaaaaagg agacttgag ggcctttgct taatgagcaa gaggttgtg 1320
tctcccaa aacatgagg agttcagaag ggagctatag ctacagaca gaaacctgcc 1380
cgctcacc atccctcgtg actgggagca tgtttgtc gaattttcta agaggactct 1440
cccttcaaaa atccaatttg ctcccagaat gttgtttagc ctctgagaat ctactcttt 1500

catttccatc tgtgaatgga catagatgtg ttgctcaggg atcagaaaca tcagagtcca 1560
gggcccagtg gcatggtgtt gcattagtag ttagaaaagt aattggtcag ctctactgtal 1620
aaagaaataa gtatgtagta cagtttttga aatgtcaggt ctgttctgtt gttttgtgat 1680
ctgaagactg tcaaaactgt tgataatcaa agaaaagggt ggtggttaga ataagtaaaa 1740
tttcagttag aaagatatag cttaccagtt ttccatgtgc ttaagggaag caagaatat 1800
tcaggttttg gagaactgtt gtaaaatgga attgaagcta gtgtctctca ccttcttagg 1860
tgtatcagag agaggaagtg gaaggccagt agtagcatct tcatacttac ttttgccagc 1920
ccagcctcca tttcaaaagc tttgtcttcc atcctatcca atgacatggg cagggatggg 1980
ctctgaggag gcagtgaggc cccaccttg tttgtccac tgtggtgtgt agtctccaaa 2040
cagcttaagg gtttttaagt tttctcacga ttacctccac tccactcatc tactatcagc 2100
atcagaaaag ttaacatccc tgggaccatt ctacttataa aagagatgaa ctagtgtgct 2160
ttctccctt ttccaggtgt gccatccata tacaatctcc tcttggccaa gttcaacaaa 2220
tgtttccagg gaaccccggt ggttgaggca aagtagccaa gatgtattga gtttaagttt 2280
tctagaggac aaaagtattt ctgttccctt ttccctcatg ctcatatgtt ttagctgagg 2340
cgtaaatggc caagttgagt aatatctgtg gaactgagac agagagccag ggacctatg 2400
aaccagggac cagtcctctg gggaatcaca cagtggctca gactagactg ctctatccca 2460
ccagaactct gctgctgttc atttccatca ggaccacca ggaaagcaaa taagttagcc 2520
ttctcatcat taggtcacct aatctcttgg gttgcaggat gagagcatat atagatctcc 2580
tgttttagaga gtgtgttcat aattgtagaa agggatagaa aatggaataa ccaagaggct 2640
gtgtcatttt ttaagaggat ggcaaggatg acctcaaatg agctcaacaa aactgggaat 2700
ccaaggaatg gtgctttagt ggaaagagag gtcagttgtg gtccttaaac ctcttggcac 2760
cttgtgcggg ttataaaaaca aggagctgga gtaaaattgc ccttaccctc aatccaaatg 2820
ctgtocagga tttaggagct acccaacctg tggttatatg gtgttggttt ccattttttg 2880
tttgttttgt tgtttccaaa atagccttgc - ggtactgc atggaaagtt caagcttttc 2940
ttcttgcccg ctacgggtcg gcctcttccc cgtgtcttca cagcgtccct aagggaagatt 3000
tttgagcac tctctggagc tgaggggagt gaaatttggg ccagagaagg cggaaggaag 3060
tagttttcct gtttcccttt ctcgagggtg atgtcctcag gcttcttca cacctccttc 3120

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tcattgggtgc ggctggcagt acagtcaggc tgtggaggag ggctgagaag aaaggggcac3180
tgggtccagcc ccagggtttgg tctgagacag gtacacagca gataccatcc caccttcctc3240
tctaaagaac agggccagcca cacatataac cctttcccta ctttactaat gtatccctta3300
tgtgggtacca gcaatggagg acaggcagac ttaccccctg ccactctagag agaattgtgt3360
tattaccogt aaaacttgac cacccccata tcccactcct ttttgtaaaa acaaatgctt3420
aaacctgtga gcttgccgtt cctttctatg tgttaatcag tttccttcca tttgagctgt3480
gtgggaggga agggcattga aattgtaggt tgtaatcttg tgccaaccaa taaaaaccag3540
tatttcacac acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3588

```

(2) INFORMATION ON SEQ ID NO. 99:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

tggtggcgtt taaataacaa atctgctaaa gttaggcaac aggcagctga cttgattttct 60
cgaactgctg ttgtcatgaa gacttgtcaa gaggaaaaat tgatgggaca cttgggtgtt 120
gtattgtatg agtattttggg tgaagagtac cctgaagtat tgggcagcat tcttgaggca 180
ctgaaggcca ttgtaaatgt cataggtagt cataagatga ctccaccaat taaagatctg 240
ctgcctagac tcacccccat cttaaagaac agacatgaaa aagtacaaga gaattgtatt 300
gatcttgttg gtcgtattgc tgacagggga gctgaatatg tatctgcaag agagtggatg 360
aggatttgct ttgagctttt agagctctta aaagcccaca aaaaggctat tcgtagagoc 420
acagtcaaca catttggtta tattgcaaag gccattggcc ctcatgatgt attggctaca 480
cttctgaaca acctcaaagt tcaagaaagg cagaacagag tttgtaccac tgtagcaata 540
gctattgttg cagaaacatg ttcacccttt acagtactcc ctgccttaat gaatgaatac 600
agagttcctg aactgaatgt tcaaaatgga gtgttaaaat cgctttcctt cttggttgaa 660
tatattggtg aaatgggaaa agactacatt tatgcccgtaa caccgttact tgaagatgct 720
ttaatggata gagaccttgt acacagacag acggctagtg cagtggtaga gcacatgtca 780
cttgggggtt atggatttgg ttgtgaagat tcgctgaatc acttgttgaa ctatgtatgg 840
cccaatgtgt ttgagacatc tctcatgta attcaggcag ttatgggagc cctagagggc 900
ctgagagttg ctatttgacc atgtagaatg ttgcaatatt gtttacaggg tctgtttcac 960
ccagcccggg aagtcagaga tgtatattgg aaaatttaca actccatcta cattggttcc1020
caggacgctc tcatagcaca ttaccaaga atctacaacg atgataagaa ccaccttaata1080
atccggttaa tgaaccttgg cctatagctt agtaatttta agtggtttat tttggtggtt1140
aatgccact gcttcacacc ttaaacttgc tttgagttgg tgggtgtacc tttaaacatg1200
catatcagtg gtgactgg 1218

```

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

gtgctcaaga agtgccttga gttggtgtac agtgccatgg ccagcaagaa tcccagattt 60
cagggtttat tacaaaatgt aagtggtcac ttggcgattt tgtagtacat gcatgagtta 120
ccttttttct ctatgtctga gaactgtcag attaaaacaa gatggcaag agatcgttag 180
agtgcacaac aaaatcacta tcccattaga cacatcatca aaagcttatt tttattcttg 240
cactggaaga atcgtaagtc aactgtttct tgaccatggc agtgttctgg ctocaaatgg 300
tagtgattcc aaataatggt tctgttaaca ctttggcaga aaatgccagc tcagatattt 360
tgagatacta aggattatct ttggacatgt actgcagctt cttgtctctg ttttggatta 420
ctggaatacc catgggccct ctcaagagtg ctggacttct aggacattaa gatgattgtc 480

agtacattaa acttttcaat cccattatgc aatcttgttt gtaaatgtaa acttctaaaa 540
atatggttaa taacattcaa cctgtttatt acaacttaa aggaacttca gtgaatttgt 600
ttttattttt taacaagatt tgtgaactga atatcatgaa ccatgttttg atacccttt 660
ttcacgttgt gccaacggaa taggggtgtt gatatttctt catatgttaa ggagatgctt 720
caaaatgtca attgctttta acttaaatta cctctcaaga gaccaaggta catttacctc 780
atttgtgtata taatgtttta ttttgtcag agcattctcc aggtttgcag ttttatttct 840
ataaagtatg ggtattatgt tgctcagtta ctcaaatggg actgtattgt ttatatttgt 900
accccaaata acatcgtctg tactttctgt tttctgtatt gtatttgtgc aggattcttt 960
aggctttatc agtgtaatct ctgcccttta agatatgtac agaaaatgtc catataaatt 1020
tccattgaag tcgaatgata ctgagaagcc tgtaaaagagg agaaaaaac ataagctgtg 1080
tttccccata agttttttta aattgtatat tgtatttgta gtaatatcc aaaagaatgt 1140
aaataggaaa tagaagagtg atgcttatgt taagtcctaa cactacagta gaagaatgga 1200
agcagtgcaa ataaattaca tttttcccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
atacgttgga atgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1303

```

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

tgaaaaaatgc ggacagtata ttcagaaagg ctattccaag ctcaagatat ataattgtga 60
actagaaaaat gtagcagaat ttgagggcct gacagacttc tcagatacgt tcaagttgta 120
ccgaggcaag tcggatgaaa atgaagatcc ttctgtggtt ggagagttaa agggctcctt 180
tcggatctac cctctgccgg atgaccccag cgtgccagcc cctcccagac agtttcggga 240
attacctgac agcgtccac aggaatgcac ggtaggatt tacattgttc gaggcttaga 300
gctccagccc caggacaaca atggcctgtg tgacccttac ataaaaataa cactgggcaa 360
aaaagtcatt gaagaccgag atcactacat tccaacact ctcaaccag tctttggcag 420
gatgtacgaa ctgagctgct acttacctca agaaaaagac ctgaaaattt ctgtctatga 480
ttatgacacc tttacccggg atgaaaaagt aggagaaaca attattgatc tggaaaaccg 540
attcctttcc cgctttgggt cccactgccg cataccagag gagtactgtg tttctggagt 600
caatacctgg cgagatcaac tgagaccaac acagctgctt caaatgtcg ccagattcaa 660
aggcttccca caaccatcc tttccgaaga tgggagtaga atcagatatg gaggacgaga 720
ctacagcttg gatgaatttg aagccaacaa aatcctgcac cagcacctcg gggcccctga 780
agagcggctt gctcttcaca tctcaggac tcaggggctg gtccctgagc acgtggaaac 840
aaggactttg cacagcacct tccagcccaa catttccag ggaaaacttc agatgtgggt 900
ggatgttttc cccaagagtt tggggccacc aggcctcctt ttcaacatca caccgccgaa 960
agccaagaaa tactacctgc gtgtgatcat ctggaacacc aaggacgtta tcttggacga1020

gaaaaagcatc acaggagagg aaatgagtga catctacgtc aaaggctgga ttcttgcca1080
tgaagaaaaac aaacagaaaa cagatgtcca ttacagatct ttggatgggtg aagggaattt1140
taactggcga tttgttttcc cgtttgacta ccttccagcc gaacaactct gtatcgttgc1200
gaaaaaagag catttctgga gtattgacca aacggaattt cgaatccac ccaggctgat1260
cattcagata tgggacaatg acaagttttc tctggatgac tacttgggtt tccatagaact1320
tgacttgctg cacacgatca ttcttgcaaa atcaccagag aaatgcaggt tggacatgat1380
tccggacctc aaagccatga acccccttaa agccaagaca gcctccctct ttgagcagaa1440
gtccatgaaa ggatgggtggc catgctacgc agagaaagat ggcgcccgcg taatggctgg1500
gaaagtggag atgacattgg aaatcctcaa cgagaaggag gccgacgaga ggccagccgg1560
gaaggggagg gacgaacca acatgaaccc caagctggac ttaccaaate gaccagaaac1620
ctccttccct tggttcacca acccatgcaa gaccatgaag ttcatcgtgt ggcccgctt1680
taagtgggtc atcatcggtc tgcgttccct gcttatcctg atgctcttcg tggccgtgct1740
cctctactct ttgccgaact atttgtcaat gaagattgta aagccaaatg tgtaacaaag1800
gcaaaggctt catttcaaga gtcattccagc aatgagagaa tcttgctct gttagaccaac1860
atccagtgtg attttgtgtc tgagaccaca cccagtagc aggttacgcc atgtcaccga1920
gccccattga ttcccagagg gtcttagtcc tggaaagtca ggccaacaag caacgtttgc1980
atcatgttat ctcttaagta ttaaaagttt tattttctaa agtttaaate atgtttttca2040
aaatattttt caaggtggct ggttccattt aaaaatcatt tttttatatg tgtcttcgggt2100
tctagacttc agcttttgga aattgctaaa tagaattcaa aaatctctgc atcctgaggt2160
gatatacttc atatttgtaa tcaactgaaa gagctgtgca ttataaaate agttagaata2220
gttagaaciaa ttctttatta tgcacacaa ccttgctata tttgtatgg atgtcataaa2280
agtctattta acctctgtaa tgaaaactaaa taaaatgtt tcacctttaa aac 2333

```

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

cattactggtt atatgagaaa catttttagta atttaataaa aggataatgt ttattttaaaa 60
aacctgactt ttccagagta attttggttt gcacattcat gtttattgaa gtggactaat 120
ttctataatg caaatcagag ttaaatatta aaaatttgtt aaatacaatt gacataggaa 180
ttacattaaa atattaggaa gaaacaagga caaatttaga ccttgaatcc gaagagataa 240
agcttacttg actttcaaat ggagagatga tgaaaaccca ctcatcagc ctttcagaac 300
aaaaagacag tcatctgata agagtatgac atggatgaaa tgccctacag gggccttgga 360
catctttaat ttctgcgatt atgtgaaaga ggtggacttt acagataatg gagcagaagc 420
caacattagt aaaaggaatc ccaacttctt cccatagaat tagaaacatg tgaaagtaca 480
ataaacttct tgttcaaatt accagcatca gagagcttcc catttgcatc tagaccttga 540

atztatatatt attgatcaag ttctaatttg tatgtatatt ttgtgcatat tcaccaataa 600
cagttaaaat taattatgtg ttatagttaa tatatgcacc taccttcttc cgttagtga 660
tcagtaaatg tgttattttg tcatttttcc aaagagagtg ttgtagggtt tccctgtagt 720
tcttccttta tagcttttct tctgataacc atgacttcag gagcttttaa actatctatc 780
ttgcatttgt gtctggcgga gaactagcca tcagcctcct gaagcctgcc atcattgtta 840
atgtgaggac tgggctgtct tggggctcag aaggtaaaga actatttgag cagatgtgtg 900
tgggtggcac tggattccac ccaactgcca agttagtatt gttagagatt tcattttaca 960
acacaaaaat aagcctgtgt caaagatttt aaaatcatgg aaagttaaaa tctagaaaga 1020
ccttagagaa ccagccaacc aactctctca ttttaaaagt gaaggattca tagcacagat 1080
tacttgctta agatcatcca ggaacgaaga caagaatcca aatgtacttg gggacaagaa 1140
ttagtcccca aattcagtg tcttcctagt attaaacatt gcccttttgc acaaattttg 1200
gatttcaatc ttggtatatt tcagtaaacc tgctgattta ttaggttact gggtagatga 1260
cattagaatg tagatagcgt gcacgctatg atagactctg ctaagacatg ttcccagtg 1320
ccagcagcaa tgtagatatg tgtgacagtg gtcatgtaga agttataaag cagagta 1377

```

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 315 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ataaggaatg agaagaaagg ctgtgtctta tcagtaggtg agatggaact ggtcctggta 60
gtgttgagc aggacaggca cttagttctg atgctgtggt ctttgtgat agtagagcac120
cggggttaac caccactcct ttaggctact tgtagtgaca acagaagtaa aatatttcaal80
ttattttaatt tagaatgtta tgttttactg gaacctgcaa tatgcatgta cagaattaat240
aatttttact cttttggtca agttatacta aggcaaagcc agtggattca aaagtgagac300
attgacaggc cattt                                     315

```

(2) INFORMATION ON SEQ ID NO. 104:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2355 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

atgatcatgc	cactgcactc	cattctgggt	gacagcaaga	tcttgtaaaa	aaaaaaaaaa	60
aaaaaacacc	gagtgaaaaa	ggaaagtaga	aggcagctgc	tggcctagat	gttggttttg	120
gaatattagg	tgatcctgtt	gagattcttg	atccagagca	atttcttttag	cttttgactt	180
tgccaaagtg	tagatagcct	ttatccagca	gtattttaag	tggggaatgc	aacgtgaggc	240
caactgaaca	attccccccg	tggctgccc	gatagtcaca	gtcaagggtg	gagagtctcc	300
ttccagccag	tgacctaccc	aaaccttttg	ttctgtaaaa	ctgctctgga	aataccggga	360
agcccagttt	tctcacgtgg	tttctagctt	cttcgactct	agcccaaatt	aggaagtgca	420
gaagcacatg	atggtgaaaa	acctaggatt	tggcagcctt	ccagaatggt	atggaatctg	480
aggggaagatt	tatgtttcgt	tttggaggat	agctcaagtt	gaattttctt	tccagccagt	540
taccttttca	acctacccat	actttgtaca	actcttacac	aaatacttag	ataatttatta	600
gatagccctg	aattcactct	aattataaac	agggagtgt	aactgcccc	agatgttcct	660
ggctgtggga	aaagcagctg	gagtgaagca	ctcattttcc	ataaaggtaa	caaagggcag	720
ctcagtggtt	actcaagctc	aaaagggttt	ttttaagagc	aagcattggt	taagtctgtg	780
tatactgagt	tggaaagtga	ttcagcacat	tcttttttag	tggagtga	gttctgaagc	840
ccccttttaa	cttctctctg	gtttttcatt	ataattggta	gccatctcat	gaactgtctc	900
tgactgttgt	ctctttgtgg	tcatgtgatt	gtgagcttgc	tttctgactt	gcattttctga	960
ctttatcctg	ttgttaggaa	gatagaaact	aggttttgaa	agattacatg	attcaagcga	1020
gggattttta	agtaaagatg	tattttattc	gaagaatcta	aaagataaca	gattatttgc	1080
ttatgaaaga	acaatatagt	ctgggaatcc	cagaattgtc	agccaaaggt	ctaagaagtc	1140
atctccttca	aatactttta	taagaagta	tttcgaggag	atctctgtcc	aaaaaggttt	1200
cactggcctc	cagattccag	ttatttttaa	aaagcaactt	accactaaat	ccttgagtct	1260
ccatagagta	acagtaaaga	aactgatgta	acagactctc	ctctcaaagg	atctcctctg	1320
gaagagacta	tcagcggcag	cattctccag	ggaagaccca	tcccctagt	ccagagcttg	1380
catcctggag	actaaagatt	gcactttttt	gtagtttttt	gtccaaatgc	aatcccattt	1440
ctgtgcctct	tagcatgcag	ttagattttg	acaaacaaga	ttcctaagga	atgactttat	1500
taactataat	atggttacag	ctattatata	aataratatt	ctggttatag	ttctaataatg	1560
gagatgttgt	gtgcaatgct	ggcctgtggt	ggtctgtgta	atgcttttaac	ttgtatggag	1620
gaggccaggc	tcagagctga	gatgtggcct	gaaccttccc	tgtatcgatc	ctttaattta	1680
gaactgtcaa	gatgtcaact	tctccccctc	tgctttttag	tggatatctga	catatactca	1740
aaacagataat	ttcctgggtc	catcatnaac	tgctaattct	gtattttata	agaattttca	1800
gatggacatg	tacaaatttg	aactcaaacc	atcccagctc	cagatacagg	gcagcgtgta	1860
ggtgaccaca	ccagagcctc	agcctcgggtc	cttctcagcc	gtcgggatag	gatccaggca	1920
tttcttttaa	atctcagagg	tagcagtaaa	cttttcagta	ttgctgttag	caagtgtgtg	1980
tttgccaata	gatacccatc	atactaattg	gccaagtaaa	tgttcattgc	acatctgctt	2040
ccactgtggt	cccacgggtg	ccatgaagtg	tgtgaggagc	ccctcatctg	gagggatgag	2100
tgctgcgttg	actactgcta	tcaggattgt	tgtgtgtgga	atattcatct	acataaattt	2160
tatatgcaca	gtaatttccc	tttttatatg	tcaagttaact	atttgtaaaa	gttataactca	2220
caaatttatta	taatgattac	taatatattt	tttccatgtt	tcattgcctg	aataaaaaact	2280
gtttaccact	gttaaaaaaa	aaaaagtaaa	aaggaggagg	tgggaaaaaa	aagctggggg	2340
gggggccccg	tagcc					2355

(2) INFORMATION ON SEQ ID NO. 105:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1339 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

attcggcacg agcatgaaac atgctcattt tacctaacag taaacaagta tgttttgata 60
gatatctgtt aatatgctta tagtggttaag aaatggactt gaggtcccag gagatttcat 120
tttattcacc ctgggtcagat acaataaagg ctatgagtat aaatacataa cttcctaacc 180
aggtgtaggg catgttcatg aatatcaaatt cttttgatgc tggacccaag agaggaaaag 240
ttgtagctaa atgttgattt acttataact agacgtctat gtgagaaaat atatgtatac 300
atatatatga tatgcagaag tcactttttt tatcaggctt tattctcctt acaaagccac 360
agtttaactg tctgcaacag ttggtttatg ttaatgatag acaaataccc agtgtttgtt 420
actttttcca actaccactg taatgataat ctttctcacg tatatacatg caacttcttg 480
gcttcatttc catgaagctg tttcaatata ttcagtatac tttgtcctta atgctgcttc 540
tgtaaacagt gatctctttc tttttttcat tcttatatct tcattagttc atcataaatc 600
tgtccagttg aggcctcagg accacggcat gatttcatga ctccgaagta ttttacagaa 660
acatttttta aataaggga atattttata taccagatgg ttcacaagtg atggctcata 720
gctagttttt ttttttcttc taaaaaatgt caggttttta aaatcattta ccttattaaa 780
atgaaaagtg ccatacttaa ctttttaaagg aaagacctga cttgcttttt ctctatttag 840
actgtttttg tactttacta atctttaaac tatcaggaaa aaaacaaaaa ctttatacca 900
atgatttagt aattttgagg catagggtag cttacgtagt ggaggatgtg ccaaattatc 960
tcttcaaatg ccaccttctc aattttataac taaaatagtg ttatctgact aattcctctg 1020
aattttgatg taagatctat ataggccccc aaaatgatcg tagtacatgc cagtcatttc 1080
tcagtgaagt aaatacaata ccagagtaca ttatgggttt tattgctttc ttttatggtat 1140
gacctgttaa tggggaaaaa atacatcaaa tcaaatagaa tcttatatct gtatgttaaa 1200
atagagcact taccgtgaagt cagtggcctg gatcatagcc ctggatcatt tcccagtcctg 1260
tcctgtgctg ggtggacctt ggacaaggcg ctgcagtagg tgatggctga gagcccttcc 1320
ctgttcccaa gtgccttgt

```

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3751 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

gatcgcgagc ggccctttgga atctatttgcg caaaagaagt ttcatttttg ttacttagac 60
 ctaagatcac ttattaaaaa tctttatttt ctccaagccc agcaaacgtt gacttctggg 120
 caaacctgaa aacctgaaaa tgcacttttc atgcagtttg tttgaagtta agtggaaatcc 180
 tttcaaatga cgagctgcag agaactcagc accaagggct gcctatctgt agatagctgt 240
 aaaatggaat attttttaaat gaaggcaaat aagtacttaa aagtgaagctg agcaataaaa 300
 tgggtocaata ataggttaaat gcaacagaaa cagaaggaga cctggttgcc ttatgccttt 360
 actcttacat ggaataaaatt cccaatgcat atcctatgta aaccataagt gaagggaat 420
 aaacctcgtc atgctccatg ctgtgaggtg tcccttggtt attctgtgat gacagagaag 480
 cctattttgt tttgttttca gcatctttct ctgatgtacg tttttaagga tttgtgaaga 540
 gctgttttca gtgttttaaat tagtgctatt tttccttgtt tttaaaaatg aatctcgtac 600
 tgtatcttac tatgtccata cagatgttac aaatcgacag ttttattctt agactcatgt 660
 gatccaagct gtatatacca tatataaaca ttttacatga atcatttagt tttttaattc 720
 atttactaat gctataaaat ttcctatatt accccagtaa tttgcatcag ctggtttata 780
 tactaaagca acatgttttg atgagtttct tacatcctta tcgaggaatt gggttaggaa 840
 aaaatacata attgtaaaac tgagtttgct gtattatact tttttcttg agtattagtt 900
 gtattactaa tcatagttg attaactgtc tacttaaggt caaggtacct gtatttttaa 960
 tccactaatt ttttttagt tgggaatag atttcaggtc ttttattaga ctaacatttt1020
 ttgagaagta aaattgactt catatacaaa gcctgtaatt ttaggcgaaa tgggaagcaga1080
 aatctaggaa gttgtgcttg cttgtatgtt gaggtttggtc tcagactaag taatgcatca1140
 gaattcatct gtttgaagcc tgaaataatt taggactctg attcactgac caaaagtcag1200
 tgttgacagag atttctctac cccgtatggt attttgtag attgttcaac aggaagcaca1260
 tgattgagaa catcttgga cagacaaaaa ccaactgacag atggcaaggc tcggcgattc1320
 tgatttccct tctcaaatct gctcaactcc aagagtcctg agaaactgct aaaattttgc1380
 ctctgtcact caagtcctac aaatgttate tctgtaaacct ttgagtgaa ctattccact1440
 gtctgttaca taggcactct attcactgca cctgtcaca cccagcaccc cccgcccg1500
 acattatttg aaagactggg aatttaattg ttagggacag taaatctact tctttttcca1560
 gggacgactg tccctctaa agttaaagtc aatacaagaa aactgtctat ttttagccta1620
 aagtaaaaggc tgtgaagaaa attcatttta cattgggtag acagtaaaaa acaagtaaaa1680
 taacttgaca tgagcacctt tagatccctt cccctccatg ggctttgggc cacagaatga1740
 acctttgagg cctgtaaaagt ggattgtaat ttcctataag ctgtaatagt ggaggtattg1800
 tgggttcatt tgagtaagcc ctccaaagat accattcaaa taacctggga gaatgtcata1860
 aattattcag ataattcaaca ctgcatgaat ctgattcaga ggcatgcatt tacatatgtt1920
 gccctaatta ccatttgatg atcataaata caagtgaatg acattggact tttagtaaca1980
 aacttaattt ttaaaaagggt gtagacaatg ctggttataa aaaaaaaaaa aacaggtacc2040
 aggttctgtg tgtttgcacc aagtaattga ctgtttttt gtttaataca tgtggaccat2100
 gaacagtatt cattctactt tttcaaatga tatgctgtag aaaatattcc ttgaagatgt2160
 gagattttaa aatttttccc tttcaatgct gttttaattg tatttcttac ttggtttttt2220
 tgattgatag cacagtgata aatcataata ctagacaaaa ttgtcttctc tttcaaacca2280
 gagccatata tatgtctgta tatatgggac ctactgcttc tctgaggaaa tgcataatct2340
 gttaatatca gacaaaatga gcaattggca gtgctcataa tatattccaa tttttattgg2400
 aattttcgat ggaatgttat ttcaataaag ccatgtaagg tgaaactttg ataactttt2460
 actcttcaag ttagggtaaa ttctgatcca atattcaatt catttgtgta cttccacatg2520
 caaaatgcta aattacaatg cagacattaa gaaaaagtat tgactggagg ggttgaattc2580

 cttgagaatt tattttatag tctaaatcac aaatacttta ctcaatttag tttttaaaat2640
 agtaaaactga atatttttgt tgraagccta tcagagtcaa tccttcgttt ggaattgttt2700
 tctgttttt cttactata aatcatttaa aaactgaatt cattttctta gatggcataa2760
 gtctgtctct tgagaaataa gtaaaatact cctattttca gtatctgtag cacctgaaat2820
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 tggacaataa aaatctgaaa gtattaacac ttgattttct actggggccc ttcaaacttg2940
 gttggaagaa attcaaccag aatatctaca ttagagtata atcatgtgtg ttaggaagat3000
 ggactagtta atcaagattt gttgtcactt aaattttttg tgattttttt ccaagccagt3060
 ttttttaaat tctaaatgtg ttttgaggta tgggtacatt aattgtaatg taaactatta3120
 tacaactgtt tttgcgactt tataggcagg taaattttgc tattactatt gaatacaaat3180
 gacaattcat ttatgaccac tcaaacagcg ttagtaacca tttagtgaac aaggattaaa3240
 acatccatct ggatgttaat tttgaagatg taattatat gttgttttaa tttttccagg3300
 catctgaaaa ccttatctgc tagacaatgt aagattcaca cagagttatc tgggattctg3360
 atttttttaa tagtacatat cattaaacca ttttctctaa atgtaagaag agcagaaaaa3420
 atcttataag attatcagat ttttctaatt acacagaaat gtaagaaaaa aatcccttta3480
 tattgaaaaa agatgcagtc aaagtctttt cagacatgcc caaactttga gaatttcttc3540
 aaccatctaa tgctataaag atttttgttc ttcctgttca caaccagttg tataacagaa3600
 atactagcta ctgttttccct tccgtgtgtg gaagtaatga atcattgatt atgtgacttg3660
 ttatgtattc aattaaacac taaagaataa aacattcact cctttaatta ataaaaaaa3720
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3751

(2) INFORMATION ON SEQ ID NO. 107:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 300 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```
cgctcggccc ccgaggagag atcgaggtgt acttggccaa gagtctggcg gaaaagctgt 60
atctatgtca gtacctgtg cgtccagcct cgatgacctt cgatgacctt ccgcacctct120
cagccaagat caagcccaag cagcagaagg tagagcttga gatggccatc gacacctga180
accccaacta ttgcgcgagc aaaggggagc agattgcgct gaacgtggac ggggcctgcg240
ccgacgagac cagcacgtat tctcgaagc tgatggacaa gcagaccttc tgctcttccc300
```

(2) INFORMATION ON SEQ ID NO. 108:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

gccaaccttc cctcccccaa ccttggggcc gcccagggt tcttgccgac tgctgttcc 60
tcttgggtgt cactggcagc cctgtccttc ctagaggac tggaacctaa ttctcctgag 120
gctgaggag ggtggagggt ctcaaggcaa cgctggcccc acgacggagt gccaggagca 180
ctaacagtac ccttagcttg ctttctctct cctcctttt tattttcaag ttcttttta 240
tttctccttg cgtaacaacc ttcttccctt ctgcaccact gcccgtaacc ttaccgccc 300
cgccacctcc ttgctacccc actcttgaaa ccacagctgt tggcagggtc cccagctcat 360
gccagcctca tctcctttct tgctagcccc caaaggccct ccaggcaaca tggggggccc 420
agtcagagag cgggcaactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480
cgtggccttg gccatggctc tgctgaccca acaaacagag ctgcagagcc tcaggagaga 540
ggtgagccgg ctgcagggga caggaggccc ctcccagaat ggggaagggt atccctggca 600
gagtctcccg gagcagagtt ccgatgccct ggaagcctgg gagagtgggg agagatccc 660
gaaaaggaga gcagtgtctc ccaaaaaaca gaagaagcag cactctgtcc tgcacctggt 720
tcccattaac gccacctcca aggatgactc cgatgtgaca gaggtgatgt ggcaaccagc 780
tcttaggcgt gggagaggcc tacaggcccc aggatatggt gtccgaatcc aggatgctgg 840
agtattatctg ctgtatagcc aggtcctgtt tcaagacgtg actttcacca tgggtcaggt 900
ggtgtctcga gaaggccaag gaaggcagga gactctattc cgatgtataa gaagtatgcc 960
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aggggatatt ctgagtgtca taattccccg ggcaaggcgg aaacttaacc tctctccaca 1080
tggaaccttc ctggggtttg tgaaactgtg attgtgttat aaaaagtggc tccagcttg 1140
gaagaccagg gtgggtacat actggagaca gccaaagctt gagtatataa aggagaggga 1200
atgtgcagga acagaggcgt cttctgggtt ttggctcccc gttcctcact ttccctttt 1260
cattcccacc ccctagactt tgattttacg gatattcttg ttctgttccc catggagctc 1320
cgaattcttg cgtgtgtgta gatgaggggc gggggacggg cgccaggcat tgttcagacc 1380
tggtcggggc ccactggaag catccagaac agcaccacca tctaacggcc gctcgaggga 1440
agcaccgggc ggtttgggag aagtc

```

(2) INFORMATION ON SEQ ID NO. 109:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

cggccggagg agcaggatgg agatccctgt gcctgtgcag ccgtcttggc tgcgcgcgc 60
ctcgggccccg ttgcccggac tttcggcgcc cggacgcctc tttgaccagc gcttcggcga 120
ggggctgctg gagggcggagc tggctgctgt ctgccccacc acgtctgccc cctactacct 180
gcgcgcaccc agcgtggcgc tggcctgtgg ccaggtgccg acggaccccg gccacttttc 240
ggtgctgcta gacgtgaagc acttctcgcc ggaggaaatt gctgtcaagg tgggtgggcga 300
acacgtggag gtgcacgcgc gccacgagga gcgcccggat gagcacggat tcgtcgcgcg 360
cgagttccac cgtcgctacc gcctgcgcgc tggcgtggat ccggtgcccg tgacgtccgc 420
gctgtccccc gagggcgctc tgtccatcca ggccgcacca gcgtcggccc agggcccacc 480
gccagccgca gccaaagtagg agggggctgg gccgcgcgcg caccocggga gcctcctcag 540
gctccctcta ttaaagccga tctgactccg cccagccaga tgtcccagat gcgccaagga 600
ctgtcctctc acccactcct ggattctgcc ctgacctcca tcctggacac tgcttgata 660
acatagaccc ttccactgac accctcgctc tcagagcccc tccagctttc cgaccccaca 720
ccgacaactc cccggcttcc agaccctacc agcactacc taacctcag ccgacagtct 780
cagccccacc gaccacttt cttggcatat agcccactt aagacccctc ctctacttcc 840
ttctgagtc tctacaaaga catccgggta ctacatttcc atcccttccc tattttgaca 900
ccaaattatg gtgtagacag ccctggccca accccaggcc agtcaggcac aatcccccca 960
cccccaaac gtcctggact gcacagacct cccactccag accatccagg cctggttccc1020
aagaccgat ctttccctg caaccagaca gtctacaact gccccctcca gccattttc1080
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cttgacacc aggccaaacta gaacacccaa caccaaactg tacagactct cccacccaa1200
cctccccaga ctctgcacgg atgtcctagg cccctcccc aactctaacc agaccccatc1260
cccctaagtc ctttgtctt gacccccaag tcttcaacca gatatcctcg gcaacccacc1320
tcccaccctc ctctcttct cttcaagac ccaactgagc acccgctctg attccccaca1380
gcctttctcc ctgccaccac tcccttagtc tttcccaggc ttactctccc aataaatgtg1440
ctagagctct gccaaaaaaa agaaaaaaa gtcgacgcg ccggaatt 1488

```

(2) INFORMATION ON SEQ ID NO. 110:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 783 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

aacatattgt tgaaaggtaa tttgagagaa atatgaagaa ctgaggagga aaaaaaaaaa 60
aaagaaaaga accaacaacc tcaactgcct actccaaaat gttggtcatt ttatgttaag120
ggaagaattc caggggatgg ccatggagtg tacaagtatg tgggcagatt ttcagcaaac180
tcttttccca ctgtttaagg agttagtggg ttactgccat tcacttcata atccagtagg240
atccagtgat ccttacaagt tagaaaacat aatcttctgc cttctcatga tccaactaat300
gccttactct tcttgaaatt ttaacctatg atattttctg tgcctgaata tttgttatgt360
agataacaag acctcagtg cttcctgttt ttcacatttt ccttttcaaa taggggtctaa420
ctcagcaact cgcttttagt cagcagcctc cctgaagacc aaaattagaa tatccatgac480
ctagttttcc atgctgtgtt ctgactctga gctacagagt ctggtgaagc tcacttctgg540
gcttcactcg gcaacatctt tatccgtagt gggtaggtt gacactagcc caatgaaatg600
aattaaaagt gaccatagg yctgagctct ctgtgggctg gcagtcctgg aagccagctt660
tccctgcctc tcatcaactg aatgagggtc gcatgtctat tcagcttcgt ttatttttca720
agaataatca cgctttcctg aatccaaact aatccatcac cgggggtggg ttttaagtgg780
gct 783

```

(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

tctgttctgt ggacaactgt tactgttctt ccgtggccaa ccatggcggc caccagccct 60
accccgcgtc cggccacttt ccctggacag tgccctcgca ggagtactca caccgcgtcc 120
cgccacacc ctccgtcccc cagtccttcc ccagcctggc ggtcagagac tggcttgacg 180
cctcccagca gcccggccac caggatttct acagggtgta tgggcagccg tccaccaaac 240

```

```

actacgtgac gagctaacgc cacgcaggcg gcggggcgct ggggaatctt cctccccagc 300
ccccgggctc gggagttatg catccagaga cctgcccttc taccttcttc gctccccctc 360
ttcttcattc cattgccccca ggtcttttcc ttttggtatt tggtttggtt ttggctttgt 420
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ggccaggacg gcaggtggcc ctggagatgg gaaagtgtct gtgtcgaggc gctgagctct 540
ctctctgttt ctcttttttt cctctactcc ttcccttcca cccccctg gctggaagga 600
acctcggttt ccctgaaaagc ttgggggtcc cacccttctt accccacccg ggaggaacgc 660
ccagggcccc gggcttgttt ctctcttgtt tttccttttg ggcagtttga tctactgatcg 720
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ccaagaatga tttctcctgc ttcttctctc tcaccatctt cccagacgga gttcaaaggc 840
cacttctcaa gcagcttttg gcaccttcag cctcagagtg gaatctttta aagacaggac 900
ccctatgtcc aggaaagggg aaaaggaact ttgccaatga tagtgaccac agcaaaagca 960
aataataata atattaataa taataaaaaga gaaaaaaaaa aatagaataa aaaaccaata1020
gcacagcccc ttgttgaagg tccag                                     1045

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(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

cacactcact gccatgaag gaagaggggg caagtgtacc gaggaagggg atgcctcaca 60
gcaagagggc tgcaccttag gttctgacct catctgcctc agtgagagcc aggtttctga 120
ggaacaagaa gagatgggag ggcaaagcag cgcggccag gccacggcca gtgtgaatgc 180
agaggagatc aaggtagccc gtattcatga gtgtcagtgg gtggtggagg atgctccaaa 240
cccggtatgc ctgctgtcac acaaagatga cgtgaaggag ggagaagggtg gtcaggagag 300
tttcccagag ctgccctcag aggagtgaag gggacaattt ggctgaagtc tttctctgaa 360
aaaagccaaa gggttatagg ggtacactta ggggttgcat gcaagctgtt accaaaaaat 420
ttttaagtat tttcttaatt tgaataataa aaccagagga aatgcataca gggcatgagc 480
aactgaggca aacctttgtg gacatgaatt gttctacgat gaatttttgc tttagtattt 540
taataagaat tacaaagaca atggcatact tggggtgaga gggagctgag gatgtctgag 600
gaggggaatag tattgcaggg aagactgaga aaacagtagg atgacagttt tgagtatact 660
ctgcactttt caattgtgca atcttcttgt gcactttaag gctttttaat tttgtttgag 720
aatgcaaatg tatactgtaa gtctaccttt actatctact atgcctactt caccatctct 780
taaggactcg gcattttgtc acagtcagac tgcaagagag ggtaggtcat gaacagtcac 840
ccgtgctggc tgtagcccc acagaggcaa tcatgccc aa tagattcaag agaagctaag 900
cggaaatgga ggggtggaagg tgtgatctgt gggactgtct gggcctgtta ctcatcctgc 960
tatcaatttc ttattaatta atcttgatga ttcttattaa ttaatcacat ttgcaggaaa1020

ttcagatgag gcaagaaaat tttattggcc tgggtaagac tgaaagcatt ccaattagg1080
cttagactgt gcaaggggct tagctaagtt atcgagctta aaaccgtca attaaacaa1140
cattatttga acagttactg catgccacgc actgtgttgg gcttagtaat aaaaaaaga1200
aaagataagt gcttgttcta gcataaatta aaaggtccaa gggaatttaa tctggaagag1260
aacatatgcc aattttttaa ctatgacagc ttttttttcc tctttccatt caaataggcc1320
cgggttcagt ccagaaaggg cacaaaatga atgaataaat aaataaatga ataaagacaa1380
aaaaaa

```

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1747 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ccagtctgtg agcccttgtc ctgtgggtcc ccaccgtctg tcgccaatgc agtggcaact 60
ggagaggcac acacctatga aagtgaagtg aaactcagat gtctggaagg ttatacgatg 120
gatacagata cagatacatt cacctgtcag aaagatggtc gctggttccc tgagagaatc 180
tcctgcagtc ctaaaaaatg tcctctcccg gaaaacataa cacatatact tgttcatggg 240
gacgatttca gtgtgaatag gcaagtttct gtgtcatgtg cagaagggtg tacctttgag 300
ggagtttaaca tatcagtatg tcagcttgat ggaacctggg agccaccatt ctccgatgaa 360
tcctgcagtc cagtttcttg tgggaaacct gaaagtccag aacatggatt tgtggttggc 420
agtaaatata cctttgaaag cacaattatt tatcagtgtg agcctggcta tgaactagag 480
gggaacaggg aacgtgtctg ccaggagaac agacagtggg gtggaggggt ggcaatatgc 540
aaagagacca ggtgtgaaac tccacttgaa tttctcaatg ggaaagctga cattgaaaac 600
aggacgactg gacccaacgt ggtatatccc tgcaacagag gctacagtct tgaagggcca 660
tctgaggcac actgcacaga aaatggaacc tggagccacc cagtccctct ctgcaaacca 720
aatccatgcc ctgttccctt tgtgattccc gagaatgctc tgctgtctga aaaggagttt 780
tatgttgatc agaatgtgtc catcaaatgt agggaaggtt ttctgctgca gggccacggc 840
atcattacct gcaaccccga cgagacgtgg acacagacaa gcgccaaatg tgaaaaaatc 900
tcattgtgtc caccagctca cgtagaaaat gcaattgctc gaggcgtaca ttatcaatat 960
ggagacatga tcacctactc atgttacagt ggatacatgt tggaggggtt cctgaggagt 1020
gtttgtttag aaaatggaac atggacatca cctcctatct gcagagctgt ctgtcgattt 1080
ccatgtcaga atgggggcat ctgccaacgc ccaaagtctt gttcctgtcc agagggctgg 1140
atggggcgcc tctgtgaaga accaatctgc attcttccct gtctgaacgg aggtcgctgt 1200
gtggcccctt accagtgtga ctgcccgctt ggctggacgg ggtctcgctg tcatacagct 1260
gtttgccagt ctccctgctt aaatggtgga aaatgtgtaa gaccaaaccg atgtcactgt 1320
ctttcttctt ggacgggaca taactgttcc aggaaaagga ggactgggtt ttaaccactg 1380
cacgaccatc tggctctccc aaaagcagga tcactctctc tcggtagtgc ctgggcatcc 1440
tggaacttat gcaaagaaaag tccaacatgg tgctgggtct tgtttagtaa acttgttact 1500

tggggttact ttttttatct tgtgatatat tttgttattc cttgtgacat actttcttac 1560
atgtttccat ttttaaatat gcctgtatct tctatataaa aattatatta aatagatgct 1620
gctctaccct cacaaaatgt acatattctg ctgtctattg ggaaagttcc tggtaacat 1680
ttttattcag ttacttaaaa tgatttttcc attaaagtat attttgctac taaataaaaa 1740
aaaccgc
1747

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(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

cgagcccaca ggccccggag tagcagcggg gagggccggga gcccgcgggc cggagccgcc 60
cggccgagggc gtgggggctg cggggccggc ccattccgtgg gggcgacttg agcgttgagg 120
gcgcgcgggg aggcgagcca ccattgttcag ccagcagcag cagcagcagc tccagcaaca 180
gcagcagcag ctccagcagt tacagcagca gcagctccag cagcagcaat tgcagcagca 240
gcagttactg cagctccagc agctgctcca gcagtcccca ccacaggccc gttgccatgg 300
tgtcagcggg ggtccccgcg agcagccaca gcagccgctt ctgaatctcc agggcaccaa 360
ctcagcctcc ctctcaacg gctccatgag gcagagagct ttgcttttac agcagttgca 420
aggactggac cagtttgcaa tgccaccagc cagctatgac actgccgggc tcaccatgcc 480
cacagcaaca ctgggtaacc tccgaggcta tggcatggca tccccaggcc tcgcagcccc 540
cagcctcaca cccccacaac tggccactcc aaatttgcaa cagttctttc cccaggccac 600
tcgccagtcc ttgctgggac ctctcctgtg tgggggtccc atgaaccctt cccagttcaa 660
cctttcagga cggaaacccc agaaacaggc ccggacctcc tctctacca ccccaatcg 720
aaaggattct tcttctcaga caatgcctgt ggaagacaag tcagaccccc cagaggggtc 780
tgaggaagcc gcagagcccc ggatggacac accagaagac caagatttac cgccctgccc 840
agaggacatc gccaaggaaa aacgcactcc agcacctgag cctgagcctt gtgaggcgctc 900
cgagctgcca gcaaagagat tgaggagctc agaagagccc acagagaagg aacctccagg 960
gcagttacag gtgaaggccc agccgcaggc cggatgacag taccgaaaca gacacagaca 1020
ccagacctgc tgcctgaggc cctggaagcc caagtgtctg cacgattcca gccacgggtc 1080
ctgcaggtcc aggccagggt gcagtcacag actcagccgc ggataccatc cacagacacc 1140
caggtgcagc caaagctgca gaagcaggcg caaacacaga cctctccaga gcacttagtg 1200
ctgcaacaga agcaggtgca gccacagctg cagcaggagg cagagccaca gaagcaggtg 1260
cagccacagg tacagccaca ggcacattca cagggcccaa ggcaggtgca gctgcagcag 1320
gaggcagagc cgtgaagca ggtgcagcca caggtgcagc cccaggcaca tttcacagcc 1380
cccagggcag gtgcagctgc agctgaggaa gcaggtccag acacagaactt ttccacaggt 1440
gcacacacag ggcacagcca agcttccagg cacagggagc ttcttccggg cgcggtgttc 1500
agtttcaggc caccaggggc agggcc

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1526

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

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cccgagaaaa accaatttaa tgcttctgtt ctcagcattt cacagcatgc aggactcaaa 60
tggatacaac agaagaaaac aaccacaaat ttttggaata ccctttgtcc aatgattcat 120
atattgatat ctattgacaa tcccttagaa ctttaaactc caaaaacaaa aaagtactgt 180
ggatctccct cgagccgaat tcggctcgag ggcggtcacc tggagatgag aaaggcccgc 240
ggggggggacc atgtgcctgt gtcccacgag cagccgagag gcggggagga cgctgctgcc 300
caggagccca ggcagaggcc agagccagag ctggggctca aacgagctgt cccggggggc 360
cagaggccgg acaatgccaa gcccaaccgg gacctgaaac tgcaggctgg ctccgacctc 420
cggaggcgac ggcgggacct tggccctcat gcagagggtc agctggcccc gagggatggg 480
gtcatcattg gccttaacct cctgcctgat gtccagggtg acgacctccg tggcgccctg 540
gatgccagc tccgccaggc tgcgggggga gctctgcagg tgggccacag ccggcagctt 600
agacaggcgc ctgggcctcc agaggagtcc tagcacctgc tggccatgag ggccacgcca 660
gccactgcc tcctcggcc gcagcaggtc tgtctcagcc gcacccagc caaactctgg 720
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agtataaaaag attcactgtg gcacgttttc cagaatgttc ttgctgtcgt tctgttgag 840
ctcttagtct gaggtcctct gacctctaga ctctgagctc actccagcct gtgaggagaa 900
acggcctccg ctgcgagctg gctggtgcac tcccaggctc aggtctggga gctgctgcgt 960
ctgtggtcag gctcctgct cctgccaggg agcacgcgtg gtcttcgggt tgagctcggc 1020
cgtgcgtgga ggtgcgcag gctgctcatg gtcccaacac aggtctactgt gagagccagc 1080
atccaacccc acgcttgag tgactcagaa tgataattat tatgactgtt tatcgatgct 1140
tcccacagtg tggtagaaa tcttgaataa acacttttgc cttcaaaaaa aaaaaaaaaa 1200
aaaaa                                           1205

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(i) SEQUENCE CHARACTERISTIC:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

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ggtatttcta aaacataaag aggagaatta agtcagctgc agaacaatgg ggctgattct 60
tctgcttttt ctctggaaaa tctttcattg ctttttggtg aaattttacct agagggttaca 120
accacaggat gtagcttggg ctcttatttg cttttttggg aaaccaatta agattaatac 180
aggataaagg aaaaaagcaa tctattcatt atataacaca gttgtttgta ttacttggtc 240
cctgcaaagg aaatctgttg aatgcttgca ttttgaattc ttttctaata gaacaaccaa 300
aaaaggcttc ttatggtgca gcaggaaaaa agatcatttt tatagctttg cattcttaac 360
atagcattta aagagcggca tgaattagag gaaagacatg gaacacacag gtagtcgggt 420
tgagatcatc ggcttaaaaag tatcctagga tggtaatgac ccagaagtat ttccagttgt 480
ctagtgggtg ggtatgcagg aatgagaagt gttttctttc catttcctgt tggacagggt 540
gcaatcttag cagagccact atttggaagt gataactaaa gatgcaata acatgactat 600
gccttctggt catcctagga ctatttgga tcttccaaaa ccttgtaaga ggcattgtcag 660
gcatgcagta aaagcatcta caacttcagc tgggcactgg cagcataggt ctcatcttgg 720
accatacagt ccacttttat agaagagggt ggaagttctc caaaacaata tccacaaca 780
agtctgacct cactctgagg gagatgggaa gtgggaggaa gaaggactaa ccagctccct 840
ggagtaagag gaatttgctt tccctgtctg ccaccagggt gctatatgtg ccacctttca 900
ggttggggcc aaggaagtga tgtcagtgtg acagaaggga gagtttagacc tccagacgtc 960
agcctccctc ccatggggta ctttttcaat ctgagtgttg ttgccttagc tgtgttggta 1020
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ttaggacttt gcctcttctt ttgtccttag cataatttct aggcagagca tccacgaagt 1140
cggttttcat tgccagctca agagcgacaa tcatttacga gttcctatgt tatgttaggt 1200
gccttatgta tattatccca aatccactgc atggtttaa tacaggcact ggaatataaa 1260
tgaaaaaggt cattacagtc actgactttc tgcaggacct taacatttc tctttccaca 1320
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ctgagcattg ccactttaat cttagaatat ttatcatttt gacacatcct gttttttaga 1560
gaggaataca aacacagttt ctgcattggg agtgtaaagc ataccttgtt aggaacgtgt 1620
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atttagtatg attgttagtg gtaacatata tcaaggcttt gaattaactg ttttatttaa 1740
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ttaaataaag ccaggttat ttagctattc tagaaagtgc cgacttcttt caagaagcag 1860
gcattgtagg acagctgaga attatcacat agcctaaatt ctagcctggc agcaagagtc 1920
acatctgaga tgtccaaaaa aaaaaaaaaa aaacacctga tctacattga aaggggtag 1980
actaacgtat gtgagaccat tttcctattt gcagttacaa ggttaaagaa ctttgaaggt 2040
cattcggctg ctaagaggca tgtcgaacac tctgtgtggc tctttcacag taaacctccc 2100
taagagcaga agacacatgg ctgttagtgt ctgcgtttag atttaatttc tcaataaaag 2160
gccttgggt gcgtatcatt tcatccagtt ataaactagg gctcctgcaa gcacccccat 2220
tctaagggtg aattattgaa atcagttgct atttgatgag tcacaactgg ccagcagggc 2280
agggcatttg aagtcatggt catcaaaaag aaatgattgt tttttgaaa gctaaatgct 2340
taaaatgctt ctagagggaa gtcgtggggc gtgtgctcat tctctttaaa atcaggggtt 2400
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ccaacactgt attcccagaa acatgacctt cgctggtctt ggggtccacat atcattggac 2520
tctgggggac acaaagatgc ctgtgacact ttggtgttgc cgagttagtc aacaattatt 2580

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ctgggaaaaa gcagaattga attcttctct agatgtccta ccagggttgg ccaagggccca2640
caaagcaggc taataaatcc ccacaggatc cagacaccag gcaaaattgc tctaagaagc2700
cagttactgt catccctcta tggttctaga aaaaatagta caaaaatgac aggtcatcct2760
atgagcgtca tgccaatgaa acccoactct ctggagaagc ccttgaatca gaattatctt2820
ttttcttgat gtcgtcagat gcagccagtt tottaatttt tttaaaaact gtatgtttct2880
gtggtatgta tatttgtaca cctaactacc tggcacttgg aaatcacagc actactcaga2940
ggcaattgaa taaagagaaa ttttaatttta aatatcaagt cctgtcaaac atttctcaaa3000
cttctgattt tatcaaaggt ttgccagcca ataaagtga tcccaagtat acaggggaga3060
aagctagact cctacagggt cctagagttt aagtaatttt tttgttatta atataggtaa3120
taatttttct aatttttatt ttttggttcc aaatgtaaag ctcttctgtt ttacctctgt3180
ttatgtcatt cttgacatgt ttatctaaat tatgtgtgct ctgtgacagg tgaaatgtaa3240
atctgggata catagtcaag atatcataag gacctacttc ccagcctacc tttcttcctc3300
tacctgataa tgataatact caaaaataca acattcaaag gaaacacaaa gaaatcctgc3360
tttcacatct cctatttctt gggctcctta ataactactg atggtttggt catgaaaaaa3420
aattttttaa tcaaaagatt gtacttggcc ctgagttgaa aaaatttcaa aaatcaaaag3480
tttgacttg gccctgagtt gaaaaaaaaa attcacattc taagaataaa cagaaaaaatg3540
ttcttcttgg aagtaaataa caaaagccat agtgttttca tttgtctttt cttcaggata3600
cacggtagaa gtcagagaat ctttgatact tttatttggt gcaataatca aggccatgca3660
acaacccaaa atcaagcatt ttggttcaag tcaggatgac atgagtgggg acagaagctg3720
tggcagtcac tcaaaataat tcatgggtcc tgaggaaaag acaggagtta acgtattaag3780
tttctactat atgcaggaac tgtgttaa attttacata agttttgata atagctaaca3840
ttagctgagc acaaaatttg ggccctgatt tgtgctgagt atctttcaca gattactgct3900
tttaatcagc agtccttgtg agctaggtat gatcattatc cccatttata gattacggat3960
gagattcg
3968

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(2) INFORMATION ON SEQ ID NO. 117:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 798 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

gtaatgggaa atttggtgtg ctgaatcttc ttcctaggat attgatatat tccacgcttc 60
tagtgggtat tctgggaatt ttacctgct cagtatttgc cctagggtac tagaaagagg120
agattgtcca aacttagcag tatggtccat ctctgtaga agtggaaatg tcatacaggal80
tagcaaacac tcttggttcc tttttgccc ggcttgccc gagccggcaa cagcaacaaa240
atgtggagga tgcaatgaaa gagatgcaaa agcctctggc ccgctatatt gatgacgaag300
atctggatag gatgctaaga gaacaggaaa gagaggggga ccctatggcc aacttcatca360
agaagaataa ggccaaggag aacaagaata aaaaagtga acctcgctac agtgggtccag420
cacctcctcc caacagattt aatatctggc ctggatatcg ctgggacgga gtggacagat480

ccaatggatt tgaacagaag cgctttgcca ggcttgccag caagaaggca gtggaggaac540
ttgcctacaa atggagtgtt gaggatatgt aactttcctg aggctgtggg ggtggctggg600
ctgtggtagt gggcatagga agcgagatat ccagtggtaa cagtgtctg tgctaataat660
tggagccac acagaccagc aacttggtga atgccagttt tgaccacaga agaataattcg720
agacctgatg tttggattga ggtacctgta cttcttggg tgttgacagc agcgggtgttt780
ggtgggtttt cagaggaa

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798

(2) INFORMATION ON SEQ ID NO. 118:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

ccccctctctg tgactcagtc tctgagcgtt ttaatacagat ggtgtccccg cgggatcaaa 60
cttcagcgtc acagctgagg actggcttcg tggctcctga tgggagagca tgaacagggtg 120
gtatgtgaag cccttgagga ccagctcttc caaagtcaaa gccaaagacca ttgtgatgat 180
tcccgaactcc cagaagctcc tgcgatgtga acttgagtea ctcaagagcc agttacaggc 240
ccagaccaag gctttcgagt tctgaacca ctcagtgacc atgttgagga aggagagctg 300
cttgacagcaa atcaagattc agcagcttga agaggtgctg agccccacag gccgccaggg 360
agagaaggag gagcacaagt ggggcatgga gcaggggccg caggagctgt atggggccct 420
gacccaaggc cttcaggggc tggagaagac cctgcgtgac agtgaggaga tgcagcgggc 480
ccgcaccact cgctgcctgc agctgctggc ctgagagatc cgggacagca agaagttcct 540
gtgggaggag ctggaactgg tgcgggagga ggtgaccttc atctatcaga agctccaagc 600
gcaggaggat gagatctcag agaacttggt gaacattcag aaaatgcaga aaacgcagg 660
gaaatgccgc aaaatcctga ccaagatgaa gcagcagggt catgagacag ccgcctgtcc 720
ggagactgaa gagataccgc aggagccagt ggctgctgga aggatgacct ccagaaggaa 780
ctgagtgata tatggtctgc tgtgcacgtg ctgcagaact ccatagacag cctcactttg 840
tgctcggggg cctgtcccaa ggcctcgagc ctaagaggcc acaaggggca ccagtgcctg 900
agccctccac tcccctcctg ggactctgac tccgactctg accaggacct ctcccagcca 960
cctttcagca agagcgcgac ccccttccca ccgcttgag cagccgggac tgctctccct1020
gaagaccct ccagagagaa aataaactag cccagaccct cctctaaa

```

1068

(2) INFORMATION ON SEQ ID NO. 119:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 4584 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

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ctcgagccgc tcgagccgcg gaagtaattc aagatcaaga gtaattacca acttaatggt 60
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agctgaccca ggtgctacac agaagtggat tcagtgaatc taggaagaca gcagcagaca 180
ggattccagg aaccagtgtc tgatgaagct agggcttggg gcaagagggc aagcagcagt 240
tggtggtgaa gataggaaaa gattccagga gccagtgcga tttggtgaag gaagctagga 300
agaaggaagg agcgctaacg atttgggtgg gaaaagagga attgggagtg gtaggatgaa 360
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gaagaaaaaa atagagaaga tagggaaatt agaagataaa aacatacttt tagaagaaaa 480
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aagctaaggg caaaatgtac aaacttagaa gaaaattgga agatagaaac aagatagaaa 600
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agaagtatag aagatagaaa aatataaagc caaaaattgg ataaaaatagc actgaaaaaa 720
tgaggaaatt attggttaacc aatttatctt aaaagcccat caatttaatt tctggtggtg 780
cagaagttag aaggtaaagc ttgagaagat gaggtgtgtt acgtagacca gaaccaatct 840
agaagaatac ttgaagctag aaggggaggt tgggttaaaaa tcacatcaaa aagctactaa 900
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 gcaaaggaag tggcttaatt atcctgaagg gatttcttct gatggtagct tttgtattat3120
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 caatgaagag gcaatgtcca tctcaaaata ctgcttttac aaaagcagaa taaaagcgaa3480
 aagaaatgaa aatgtttacac tacattaatc ctggaataaa agaagccgaa ataaatgaga3540
 gatgagttgg gatcaagtgg attgaggagg ctgtgctgtg tgccaatgtt tcgtttgcct3600
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 gaccttatat aggaaaaaga tgag 4584

(2) INFORMATION ON SEQ ID NO. 120:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 982 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

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gtggagggga ccctgtgggt agcagcagct atcgagcgt cggatgttca gagcagcaga 60
agccggcgct gtcggatgtt gtgttgcccg ccaccatgag ctacacaggc tttgtccagg120
gatctgaaac cactttgcag tcgacatact cggataccag cgctcagccc acctgtgatt180
atggatatgg aacttggaac tctgggacaa atagaggcta cgagggtat ggctatggct240
atggctatgg ccaggataac accaccaact atgggtatgg tatggccact tcacactctt300
gggaaatgcc tagctctgac acaaatgcaa acactagtgc ctcggttagc gccagtgcg360
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gcggccggcc aatggccgca ggctatgggc gcatgtggga agaccccatg gggggccggg720
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ttggttttgc ggtttggcaa tggcatgaag cagatgaggc cggactggga agacggggac900
cacagccgat ttgcgaacca agaagaagaa gagaaagcag ggcggcattc tgattgagcc960
agttagcaaa gcagccggaa tt                                     982

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(2) INFORMATION ON SEQ ID NO. 121:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 742 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

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ctcaacttcg cactgactgcg tgcctcaagc cgacgcagcg gcctactctc gcaactgcaga 60
cggggaaact gaggcccgag gcggccgggg tggggcagac ctcccggcga gcccgagccc120
ccgcccccg ctagccccgc cctggcccggt aagaagcacc cggggcgcgga ggcgaaggcg180
cacagcgcg ggcagcgctg ggtccagcag cgcgatggca gctcagcggc tgggcaagcg240
cgtgctgagc aagctgcagt ctccatcgcg ggcccgcggg ccagggggca gtcccggggg300
gctgcagaa cggcacgcgc gcgtcacct caagtatgac cggcgggagc tgcagcggcg360
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agacatgccc gatgagatca acattgatga attgttgag ttagagagtg aagaggagag480
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ctcccacgac ggcagcctca gcccctcca ggaccgggcc cggactgctc acccctgacc660
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aatggttctg taacaataaa aa

```

742

(2) INFORMATION ON SEQ ID NO. 122:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

"RECEIVED" 07/22/93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

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gtttggacaa gttgttttaa taggaaatag acotgogtgc ttcataaggtt tcctcaacca 60
cctttcctca gctttcttaa aatgggatct acattggctc ttcacaccca aatagcagac 120
taatcgtttt tctgcttagc accgtctggt tcattgtctt gaactctgcc ttacagcagc 180
aagaaaatth tctcgcacaa gaacctcaat ctttagttcc attgagctcc ccctctggat 240
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aggtctgaag aggagactac caaagcagtg tttacaaacc cagagtccac acaaccatat 360
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```

(2) INFORMATION ON SEQ ID NO. 123:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

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gtggaagtcc atggtgagca cggcagtggt aagtcgccag aaggagagac actcgggtgag 180
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gatcaaggaa caatgtcccc tggaagcagg actgcatagt agcagcaaag tcacaataca 660
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caggccactc ccggaggggt cgatcctctg aagcttgaga tctatctcac cgacgaagac 1320
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ttcaggagggt tatcagaatt aataaaagta tctgttatgt gcacttaagc cgcagctgct 1680
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ttctctttat aaagtgttat tttgatagtt tgtggattct aaaataccat ataagtcaaa 1800
tatggattta acaaagcaat atgtattcat tcactttcga gatttggggg gttgtttttt 1860

(2) INFORMATION ON SEQ ID NO. 124:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 807 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

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cctttcctca tctctattaa attgtaaaca ggactactgc atgtactctc tttgaggtga 60
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caatatatga aatagtaccc tctaaaaaag agaaaaaaaa aatcaggcgg tcaaacttagl80
agcaacattg tcttattaaa gcatagttta tttactaga aaaaatttaa tatcaaggac240
tattacatac ttcattacta ggaagttctt tttaaaatga cacttaaaac aatcactgaa300
aacttgatcc acatcacacc ctgtttatct tccttaaaaca tcttggaagc ctaagcttct360
gagaatcatg tggcaagtgt gatgggcagt aaaataccag agaagatgtt tagtagcaat420
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tggttcactg gcttaagagg tttctcagaa tatctatggc cacagcagca taccagttt660
ccatccta at aggggaatgga aattaatttt gtaacctact gattaacaga atctgggggt720
cacattggaa aaaaattctt ttatccgtct ttaaggata tgtttaataa ttattttatg780
tgtcggcata ttgcggacag tctgaga                                     807

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(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1932 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ccgggggtttt gggctggaac tgcagcgctt agagagctcg gtggaagctg ctaaaggcgg 60
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ttcagccccc agctggattc cagccattgc tgcagctgct ccacagccct tttcaggacc 180
caaacaaccg cagccgctgt tcccaggatg gtgatccgtg tatatattgc atcttctct 240
ggctctacag cgattaagaa gaaacaacaa gatgtgcttg gtttcctaga agccaacaaa 300
ataggatttg aagaaaaaga tattgcagcc aatgaagaga atcggaagtg gatgagagaa 360
aatgtacctg aaaatagtcg accagccaca ggtaaccccc tgccacctca gattttcaat 420
gaaagccagt atcgcgggga ctatgatgcc ttctttgaag ccagagaaaa taatgcagt 480
tatgccttct taggcttgac agccccacct ggttcaaagg aagcagaagt gcaagcaaag 540
cagcaagcat gaaccttaag cactgtgctt taagcatcct gaaaaatgag tctccattgc 600
ttttataaaa tagcagaatt agctttgctt caaaagaaat aggtttaatg ttgaaataat 660
agattagttg ggttttcaca tgcaaacatt caaaatgaat acaaaattaa aatttgaaca 720
ttatggtgat tatggtgagg agaatgggat attaacataa aattatatta ataagtagat 780
atcgtagaaa tagtgttgtt acctgccaag ccattcctgta tacaccaatg attttcaaaa 840
gaaaacaccc ttccctcctt ctgccattac tatggcaact taagtgtatc tgcagctcta 900
cattaaaaag gagaaagaga aataacctgt ctctcattcc taagttgcct cattaatatt 960
catgaacaag aatatgtacc tttttgatgc tatattactg cgattaaaaa gttcttgcag 1020
gtaatgttta tgatatgtta aacgttgtaa tttcttatcg taattataac attcccattc 1080
ttttgtagat gaaacttcta catattgaac cacagatttt ctgagcttct aaatgtagcc 1140
tttcattgca catttcagtg atcagaatag atatcctttt acacgcacaa aagcaataga 1200
ttcattcagt ggacaagttc cttgtttaac tacacagcta tgatggaatg atatatccaa 1260
gttccttgcc tcagtgaat atgcatatgt atatcatgaa agtgggatgc caagtaagct 1320
taaaatggca ttctctagca aagagattag actttttaa aactottata aaacagggtg 1380
gcgatcattt cccaagattg gtttcccttg agtttttgct aaaacaaatc ttagtagttt 1440
tgcccgttta aaacaactca caatcgtaa tgctactatt cctaagatat cttacctttt 1500
tatttcagtt tagccatgta ttgtatgagt gtattagtct aagcagtgag aatcttttct 1560
atgcctctat tccagcaaaa agtagaagta tcaaataaaa agggcaactt ttaaaatatt 1620
aagcctgaag acttctaaaa agacaagaaa catggcctaa ataaccaaca tagatttaca 1680
tagtaagttt cacactacct tattacaaa agcaaacacc tcttacttta aactacatta 1740
tcatgtatat ctattgtatg ctggtcttta ctttttgcca aaatcaacat ataatgaaga 1800
gatgcctttg tttcatgaga ttcaaaactg atgctatgct ttaaaataaa ctcagtactt 1860
ttagaaacat aaaaaaaaaa aaaaaaaggc gacccccga gtagtggggc cgcgcccggg 1920
gatttttccg gg
1932

```

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

atatatgtta agacattccc ttgctaatta ttttcttctc tgttgttcta tttttttggt 60
ccagtttgct gtttttaaaag ttttgagtc cagctggtcc tgtacattta actgaaaaaa 120
aagtaactta aaataatata aaaatagcac tcatgtatgt cctacagtta taggtgaaat 180
ttgatattgt ttgtcttaca tagcatacct atagacagct taagtaaagt gactgttaag 240
agggttatgc ttattgatga actctttag ttgtttacca gctctgttag tatagttaa 300
ttgatctcag tagcttcaag tatttataaa atgggtgaag tccaaatata tgtgataatt 360
acaatacact ttgaattaat ggggggtggg aggctagttg aaatgcattt tatttacc 420
aggagtatgt taaaatgata gttataaatg ttggaagttt aaagcaagat actcagttta 480
gttctttaca aatcataaga agaacaaaat tagatgttga cattgctatt ttaggctgtg 540
tgttttccat atgcttcttg ctttccctgt cacagggttg ggcagcaata ttggtgtgat 600
tgaggttatg ctggcaccac tcgcacacag gcgcacaatg gtgttagctg ggcagaaaga 660
gtggcatctc tggctaccgg gctgggggcg acctttacca taggatgaag taaccttgca 720
ttcggctgca aggtgtactg tacgtacaca ggtgctggtc gatgtccact ttctgctttt 780
ctttctttct tttttctttt tttaaagtaa tttccccac agtaaaatac actgactcct 840
gagtaaattg attttccagt tttatggaat tgggagctg acaagtgaag ccaattta 900
gtaaagtatt tggctttcaa atggtttctc tgtgctattt tttggaattc tttcagattc 960
cagagatata ttacgtcttt gattcaattt aaaatttgta cttattttct tttagaaata 1020
atgtattgtg tctgtgcaga aaaaaaaaaa ccaaaaagga ttgctttact ccaagaggag 1080
agattgtctt aggataaacc tccaagctca catttaatat aacagactga agtaaacatt 1140
agaatcctgt ttagagctat tctgcacagt taactactga tctttagaat ctaaaattgt 1200
atatgaactt attcttaaat aattgaaccg ttttatattc aaatgactta tgatcggtgt 1260
tagtttgga aaaataagat ggttaaattt tgatttattg aaatgtaatt gtattatttt 1320
cataaaatag cattttcatt ttgtaatgtg gtttaacatc cttgttggtt gccaaagaaa 1380
tttcatttgg ctgtgaatat tctatttgct tgcagtatct gtttctcttc ctaggctcaa 1440
gttggtgacc caagcctatt gtaaacaagt gattatctca aaggagatg ccaatggagt 1500
aacaatttgt taaccttacg ttttctgtct gtatattttt ttaaaaatct ggtagtttct 1560
ggaaaaaaaa gagaaggggg tttgtagtac ttaacctat ttatttccgt atattttagt 1620
taattagttt ttggaataaa tggatttcag tatagctttg tggttaaatt gcattgcctt 1680
tattttatgt ttaggcttat ttttaaatta acatttaaca gaaacatttg aaatagaatt 1740
tgcattgtct ccttaattaa cttaaagact gattttaatc tgactatgac actgagcata 1800
ttctttaaat tactcataat ttataatgct taatataatc ttaattaaat ttagcagttt 1860
tagtataaga tgtgccattt tgtcctctgt atgtctgaat gaagctataa catttgcctt 1920
tttattgcag gttttccttt ggaatatgga taaatacacc atgatacgga aactagaagg 1980
acatcaccat gatgtggtag cttgtgactt ttctcctgat ggagcattac tggctactgc 2040
atcttatgat actcagatat atatctggga tccacataat ggagacattc tgatggaatt 2100

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tgggcacctg tttcccccac ctactccaat atttgctgga ggagcaaatg accgggtgggt2160
acgatctgta tcttttagcc atgatggact gcatgttgca agccttgctg atgataaaat2220
ggtgaggttc tggagaattg atgaggatta tccagtgcaa gttgcacctt tgagcaatgg2280
tctttgctgt gccttctcta ctgatggcag tgttttagct gctgggacac atgacggaag2340
tgtgtatttt tgggccactc cacggcaggt ccctagcctg caacatttat gtcgcatgtc2400
aatccgaaga gtgatgcccc cccaagaagt tcaggagctg ccgattcctt ccaagctttt2460
ggagtttctc tcgtatcgta tttagaagat tctgccttcc ctagtagtag ggactgacag2520
aatacactta acacaaacct caagctttac tgaattcaat tatctgtttt taaagacgta2580
gaagatttat ttaatttgat atgttcttgt actgcatttt gatcagttga gcttttaaaa2640
tattatttat agacaataga agtatttctg aacatatcaa atataaattt ttttaaagat2700
ctaactgtga aaacatacat acctgtacat atttagatat aagctgctat atgttgaatg2760
gacctttttg cttttctgat ttttagttct gacatgtata tattgcttca gttaggccac2820
aatatgtatc tttgctgtaa agtgcaagga aattttaaat tctgggacac tgagttagat2880
ggtaaatact gacttacgaa agttgaattg ggtgaggcgg gcaaatcacc tgaggtcagc2940
agtttgagac tagcctggca aacatgatga aacctgtct ctactaaaaa tacaaaagaa3000
aaaaaaaaaa aactcgaaac tact
3024

```

(2) INFORMATION ON SEQ ID NO. 127:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 505 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ctgcacgggc gcagatgtag gcaccgggtcc gagtgcctgc cctctgtccc cgcggctggg 60
tctcgtctgc tccggttcct gggctcctaa ttcttggtcc agcttcttcc aggtctgcgc120
gtctgttgtt cccagcgctc tgcgaagctg aaaaggagga gcaacctgtc cagaatcccc180
gcaggacagg aaaaggaggg gaaatctcga catggaaaaa ctctacagtg aaaatgaagg240
aatggcttca aaccaaggaa agatggaaaa tgaagaacag ccacaagacg agagaaagcc300
agaagtaact tgtactctgg aagacaagaa gttagaaaaa gagggaaaga cagaaaacaa360
gggcaaaaaca ggagatgagg aaatgttaaa ggataaagga aagccagaga gtgagggaga420
ggcaaaagaa ggaaagtcag agagggaggg agagtcagag atggaggagg tcgagagaga480
gggaaccgca ggtaggggaa gcgga
505

```

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

PPLLRLFFFY LRKFISTSTA EIRKWYRFGQ IILYEMDPHT TSFLIQARYN IIPGFSKSSQ 60
 HGILCYSVLA FIAASSFERRA FFSKFKLVKV SCLWAAFLPS ITMKMHPTTV RAIIR 115

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

VRDGAPGLSC GFVQNPFILE KSELLVSLRD EETSLSHNLK QLPAARRRPL RLPATCYSA60
 DQRTSPGTV ALVSSMSPSV GV 82

(2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GIITLSLLMI IHPQMEEFIR QPLQFRLKTG AHRTQGTIKE DQEPRFFLSK NWP

53

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

LFILRWRSLS VSHFSFVLKQ EPTGPKELLR RTRNLGFFFQ KIGPSPINEG KN

52

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

KKKPRFLVLL NSSLGPGVSC FKTKLKWLTQ KLLHLRMNNH Q

41

"B9999" B9999

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

ADPAFSTDLF QGCTDMAAAF RKAAKSRQRE HRERSSDYRK KQEYLKALRK KALEKNPDEF 60
 YYKMTRVKLQ GGVHIIKETK EEVTPEQLKL MRTSGRQIYR KGRGCRS 107

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRRSPLIFS KAVQTWRRLF GRRLSPGSGN TESEAVTTVK NKNTSKLFGR RLLKKIQMNS60
 TTK 63

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

LFWGYFFLSL LNNMYSTLEF NPSHFVVEFI WIFFKSLLPK SFEVLFFTV VTASLSVFPL60
PGLSRLPKSR RHVCTALEKI SGERRIR 87

(2) INFORMATION ON SEQ ID NO. 137:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 95 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

EANNYMSCQG GSRFHSFSIL PQYPGINAAT GGQSLFVLLP TPSLFCLFNS VKLFCLGPGK60
EPKENLSGQV HFWNAENILK ARFLEYSQLA FFPLI 95

(2) INFORMATION ON SEQ ID NO. 138:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 77 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

NSSASSPQFW PNSRLAVETW YPGVGLLTLI SMMFSKMKLD KVDHQLHRVF CKSIVSKWPR60
DLRKIQIFCL PWSCEFS 77

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 133 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```
DLKQDQGGKQK ICIFLKSLGH LLTILLQKTR CSWWSTLSSF ILENIIIEIKV SNPTPGYQVK 60
TASLLLGQNC GLLAELFYGL QSKWSYLTHH MTKVLNLVRG KVLNIQFWIQ EIIIVNFFPK120
SMERMLVENI LKI 133
```

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 783 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```
FLLQPSAFHL YEPPLDYTMT WRMGPRFTML LAMWLVCGSE PHPHATIRGS HGGRKVPLVS 60
PDSSRPARFL RHTGRSRGIE RSTLEENLQ PLQRRRSVPV LRLARPTEPP ARSDINGAAV120
RPEQRPAARG SPREMIRDEG SSARSRLRF PSGSSSPNIL ASFAGKNRVW VISAPHASEG180
YYRLMMSLLK DDVYCELAER HIQQIVLFHQ AGEEGGKVR R ITSEGOILEQ PLDPSLIPKL240
MSFLKLEK GK FGMVLLKKT L QVEERYYPVP RLEAMYEV ID QGP IIRRIE KI RQKGFVQKCK300
ASGVEGQVVA EGN DGGGGAG RPSLGSEKKK EDPRAQVPP TRESRVKVL R KLAATAPALP360
QPPSTPRATT LPPAPATTVT RSTSRVTV A ARPMTTTA FP TTQRPWTPSP SHRPPTTTEV420
ITARRPSVSE NLYPPSRKDQ HRERPQTTRR PSKATSLE SF TNAPPTTISE PSTRAAGPGR480
FRDNRM DRRE HGHRDPNVVP GPPKPAKEKP P KKAQDKIL SNEYEEKYDL SRPTASQLED540
ELQGVNVPLK KAKESKKHEK LEKPEKEKKK KMKNNENADKL LKSEKQMKKS EKKSKEKEK600
SKKKKGGKTE QDGYQKPTNK HFTQSPKKS V ADLLGSFEGK RRLLLITAPK AENNMYVQQR660
DEYLESFCKM ATRKISVITI FGPVNNSTMK IDHFQLDNEK PMRVVDDDEL VDQRLISELR720
KEYGMTYNDF FMVLTVDVLR VKQYYEVPIT MKSVFDLIDT FQSRIKDMEN QKRGVFFEGG780
KTP 783
```

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

KMVVGWVWFL RWERMENLF QGNGFAAEVR MCSCIDLQTP RRWVHTACLG VPRDSRPPTY60
LSEARAAGHG PSAKPVCDAL GALVQEA 87

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SFSSLGVRNT LFITFKFALY FFSSMLVLWT FGDVSVRAGE RGVRRPSHRW SWPPPALSSL60
PDHREFPICPS ENLSQGELKF TGQGTSTFIYF IMLANRT 97

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

87

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 119 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

NSKDKCFSLA  FITTPETERW  RCCASEPRLL  ALKHQGHRTQ  AWQRGHGQRH  ELQTSMLEVS  60
NPLAPPSMQC  APTFWVSADR  YRNTSLPLQR  THFPGKDFHT  SSPTSCKPTH  PQPFKAPR    119

```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 87 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

87

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

DPPSHSQLGR CCHRMVFESV GARAHFWLSQ QLGWHLPSA RNSNIMNARD SVLSKVFPK60
GAGHGCSRL 69

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

SAHLGLPKCW DYRREHPCPA PFGWKTLLST LSLAFIMLLF LALGSKCHPS CCDNQKCALA60
PTLSNTIR 68

(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

HHTQPIFVFL VATGFHHVGQ AGLEPLTSGD PPTLASQSAG ITGVSTRALP LLDGRLY 57

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SAGIPKLAPK IPLPFSDLLK CYLISGAFFD HTLKTSTPTH GPCPPSRLHF LAYTYQM 57

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

LKTLLTVASI RVSTFYSSDP TSFNLLLLLIY GG

32

"1995-04-24 14:35:35"

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TKRAVMKSMH LCAIRAFVLP HSELIDSDYI HF

32

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GRVRAVKGRH SDRSHSQCF QSVNTDEVPT T

31

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

VQNVMSACNF IFIKAKLIYM EYCSIYYAPI YILSPVVRYF ISLLLNIYF YL

52

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 59 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTFCCFFICC IENSHTQFSI LCQCSHHGWT LGRNSPQPFL VSFSQFFSVS RWAPVINLP 59

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 38 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

LSLCPCWPGN FFQWCLLEEV FSSGQFKEIK LGNGEGGR

38

"1999" 09E4553

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

GSILDMMQEI SSWSQKFPRG AVFLRNGVYL NNS

33

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KKLPGQHG HK LNYLNLK LHF LKIQHLLGTF DSRKRFPASY PKCF

44

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```
AAGGLGLGVG PRGMWRAGSM SAELGVGCAL RAVNERVQQA VARRPRDLPA IQPRLVAVSK 60
TKPADMVIEA YGHGQRTFGE NYVQELLEKA SNPKILSLCP EIKWHFIGHL QKQNVNKLMA120
VPNLFMLETV DSVKLADKVN SSWQRKGSPE RLKVMVQINT SGEESKHGLP PSETIAIVEH180
INAKCPNLEF VGLMTIGSFG HDLSQGPND FQLLLSLPEE TVVKS 225
```

(2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```
CRGPGARRRS PGDVESWQHV GRAGSRVRIA GGERARAAGC GAAAAGSPSH PAPASGGQQN60
QTCRHGDRGL WTWAAHFWRE LRSQTARKSI KSQNSVFVS 99
```

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```
LRSCPKLPMV ISPTNSRLGH LAFMCSTMAM VSEGGRPCLL SSPLVLIWTI TFNLSGEPFL 60
CQELFTLSAN FTESTVSSMK RLGTAINLLT FCFCRWPMKC HLISGHKDRI LGFDAFSSSS120
```

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSTGPSSPLV ASAATELA AF AAFSSACMR PEGSASLFWN RLPLLMFGDL QGCEAREGIA60
 MRILQASFSG LSSKG 75

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

NTHGDALTCL TPLQVPKHEE GKAIPKQRGR TFRHTCR AK GSGKSCQFSC SRGYQGAGGT60
 SAGLALYLHT RTAASRGTS G SPVGSVAPQQ 90

(2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SHPFEDSPEK EACKIRMAMP SRASHPCRSP NMRRGRRFQN REAEPSGRIH AELKAAAKAA60
SSVAAEATRG LEGPVLV 77

(2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 347 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TAFPLPVVVA AVLWGAAPTR GLIRATSDHN ASMDFADLPA LFGATLSQEG LQGFLVEAHP 60
DNACSPIAPP PPAPVNGSVF IALLRRFDCN FDLKVLNAQK AGYGAAVVHN VNSNELLMV120

WNSEEIQQQI WIPSVFIGER SSEYLRLAFV YEKGARVLLV PDNTFPLGYY LIPFTGIVGL180
LVLAMGAVMI ARCIQHRKRL QRNRLTKEQL KQIPTHDYQK GDQYDVCAIC LDEYEDGDKL240
RVLPCAHAYH SRCVDPWLTQ TRKTCPIKQ PVHRGPGDED QEEETQGQEE GDEGEPRDHP300
ASERTPLLGS SPTLPTSFGS LAPAPLVFPG PSTDPPLSPP SSPVILV 347

(2) INFORMATION ON SEQ ID NO. 168:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 588 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

QVTNMSDKSE LKAELERKKQ RLAQIREEEK RKEEERKKKE TDQKKEAVAP VQEESDLEKK 60
 RREA EALLQS MGLTPESPIV PPPMSPSSKS VSTPSEAGSQ DSGDGAVGSR RGPIKLGMAK120
 ITQVDFPPRE IVTYTKETQT PVMAQPKED EEDDDVVAPK PPIEPEEEK LKKDEENDSK180
 APPHELTEEE KQQILHSEEF LSFFDHSTRI VERALSEQIN IFFDYSGRDL EDKEGEIQAG240
 AKLSLNRQFF DERWSKHRVV SCLDWSSQYP ELLVASYN NN EDAPHEPDGV ALVWNM KYKK300
 TTPEYVFHCQ SAVMSATFAK FHPNLVVG GT YSGQIVLWDN RSNKRTPVQR TPLSAAATH360
 PVYCVNVVGT QNAHNLSIS TDGKICSWSL DMLSH PQDSM ELVHKQSKAV AVTSMSFPVG420
 DVNNFVVGSE EGSVYTACRH GSKAGISEMF EGHQGPITGI HCHAAVGA VD FSHLFVTSSF480
 DWTVKLWTTK N NKPLYSFED NADYVYDVMW SPTH PALFAC VDGMRDLW NLNNDTEVPT540
 ASISVEGNPA LNRVRWTHSG RGGGCGGILK DKFCYFAM LG GAVCWSPQ 588

(2) INFORMATION ON SEQ ID NO. 169:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 41 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

FHVEQLSHSF LSWRKDTIQR GSKDFVKRGI HNLLWSKCPH L

41

(2) INFORMATION ON SEQ ID NO. 170:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 55 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CPRDVGTC SI VNYGCHVLQN PYCPFELCPS SKIRSYDSIV QHGIIMKSLS SSIFP

55

"1995-01-01" 01:01:01

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KAFVLVSFPK WALFLVIHMT LFGCGCLLNF LEWTSFSKPK PARDRKGNGN

50

(2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CTFNIESFIY LIVYRTFHNH THLLHNILTS IFKFFCTSSF SFNLVKPVIH TNVYCELG60

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

EEFVFLIHS FVNRYKGTNV LTYTKKKKIL VYPLMLIHRV LSYNVIQLGS LTFPPKNIFI60
EKGITLS 67

(2) INFORMATION ON SEQ ID NO. 174:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

LYHIIRKHSV DQHKWVHKNF FELGVCKHIC SFISVYKTVN QKDKTEFLVF VIEFLN 56

(2) INFORMATION ON SEQ ID NO. 181:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 289 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SRRTQGAAST	RFPQPDITIGQ	DFSASAQRGG	LVAHSDLDER	AIEALKEFNE	DGALAVLQQF	60
KDSLHLHVQN	KS AFLCGVMK	TYRQREKQGT	KVADSSKGPD	EAKIKALLER	TGYTLDVTTG	120
LNRYGGFPDP	SVSYGQPPSV	GTEIFVGKIP	RDLFEDELVP	LFEEKAGPIWD	LRLMMDPLTG	180
KRKYGAEVTE	CTKEAAQEAV	KLYNNHHEIRS	GKHIGVCISV	ANNRLFVGSJ	PKSKTKEQIL	240
EEFSKVTETGL	TDVILYHQPD	DKKKNRGFCF	LEYEDHKTAQ	QARRRLIEW		288

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

KLCTEWLKV G IWRWMRGSC LGRLCFTWIR VGLREEIGV

39

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

EAVMTLILIL HTYFLTQPYS NPSEAKPSQT APSHPSPYPP NL

42

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

PSFSFYTPIS SRNPTLIQVK QSLPRQLPLI HLHIPPTFNH SVHNFYSLHT SYLLIFLTNK60

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 46 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

RSRFHMMLTL RALQLSLPTK IGGACFRVSR LSPTEKKKKK MSLEEA

46

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 65 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ITFSHDAHAQ GASIIPPHKD RWRVFQGLSS LSyrKEKEKN VIRRGVTRQS VPRFVFPGVA60
ERDQF

65

"1999" 04242550

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ECREAGPLFL QSRLELISFG HSRKHKPGDG LTCYASSNDI FFFFSVGER RETLKHAPPI60
FYGRDN 66

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

RQTEGETEML RKPSYTTLPR NTSLRECKKY YWRWKSARKTA MGRRPGRD

48

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

RAETRSQGQL NEDKLGKLR CLESPAIQLY PEILPLGNVK STTGDGRAEK QLWAEQGQVI60

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SCIAGLSKHL SFPFSLSSLS CPWLRVSALQ LLPLRAFPPA SDLL

44

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIMNGLVLDN IWPBKLLTSV LGESHFVNHT SEIYMMLNGE QRRSCCKRCI KYLCCFCMRL60
RSFSHLSPLF PIRISREAKL FCGFGNGHFP GKCIWIDD

98

"00000" 01924950

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AHSSTKAKSK SEFLPILPLC NTLRSSHNCP TPHLPVSCCT KSPSLSSFRY IVRQGRRLR 60
 RRAFEALSTL PASVKMRLHY SPEKRARFSH RSRCIFPGND HSQTHRTVWL LWISL 115

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

SGVKRISCVL ETKAYCHCFK KSLCEMKKNM TNTGSHTYTY IQRNLHTCTH TGRYRHTVPP 60
 KRSPNQSSYR FYHSVILSEV PTTAQHLTYP FPAAQSLLS HLFDTSSGRA EGHYAAEHSR120
 LSAHCQPA 128

(2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(vi) ORIGIN
(A) ORGANISM: HUMAN

RRGVEPPLLR RLPDSETQKR VQGWGEMWSE GRFAFEKGSS RTHWDIVTHL NHLLIERCWP60
 PNNGRSGPGP RA

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 77 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(vi) ORIGIN
(A) ORGANISM: HUMAN

GPSPYARGPG PDLPLLGGQH LSIRRWFKCV TMSQCVLELP FSNANLPSLH ISPHPWTRFC60
VSESGNLLKR GGSTPGL 77

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(vi) ORIGIN
(A) ORGANISM: HUMAN

EANTFLSEDG SNVLQCPSVF SNFLSQMQTF PHSTSLPIPG PVSVSLSQAT FSKEGVPLPA60

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

PTTTLVIPLE FLSSRKRKQK DSFQTALCSL HCSFPKQAAS TGKAHVVTYPY FSEVLLFHGV60
 TLLSESKFRK QVLPLADKNH TSFL 84

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CDRVPLFLSY WCAVADSWLT ASSVSHVKGI LSPQTECAP PGPANCFNFF FFFFFFFLVET 60
 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQPEQD DLNLINSTPK QQLSLSQGCQ120
 GGLCEGKD 128

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRLYYKKLV WFLSAKGKTC FLNLLSDNKV60
TPWKRRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

(A) LENGTH: 49 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

PDFRGFAGPA MFSRGEFQVGR GERQGENAPC RGVQRSPASC PAVGWTSDL

(A) LENGTH: 56 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

QISGVLRA PR CFPEVFKWEE ESDKVKMPRA GASSGVLPAV RRWGGRLIYE GAHPPI 56

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CCSCQSSQVR YSDRWMTFTI NQTSTPPPD S WQDSAGRP GT GHFHLVALL F PLENLWKTSR60
GPQNPGNL 68

(2) INFORMATION ON SEQ ID NO. 209:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

WGGRTLASAV SIPLRKCHSH RPTVLARKQP QSGVPPPYTA IASPDASGIP VINCRCVQSL 60
INLDGKLHQH VVKCTVCNEA TPIKNPPTGK KYVRCPCNCL LICKDTSRRI GCPRPNCRR120
INLGPVMLIS EGTSSACIA QSQPEGYKGR VLGHGWGTHS LWDG 164

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SSAVPDGAVG RPYAVAVGGP PHSCRCRPCC LMAAIGVHLG CTSACVAVYK DGRAGVVAND 60
AGDRVTPAVV AYSENEIIVG LAAKQSRIRN ISNTVMKVQK ILGRSSSDPQ AQKYIAESKC120
LVIEKNGKLR YEIDTGEETK FVNPEDVARL IFSKMKETAH SVLGSDANDV VITVPDFDFGE180
KQKNALGEAA RAAGFNVLRLL IHEPSAALLA YGVGQDSP 218

(2) INFORMATION ON SEQ ID NO. 211:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 186 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

RKWTLTSMQ KRMLKRPDNK LKYVTKWQRT AKQITHPFSR NSTMSSMNIT ILTSPTSSRK 60
YKRAEERRIV RMGESMKTYA EVDRQVIPII GKCLDGIVKA AESIDQKNDS QLVIEAYKSG120
FEPPGDIEFE DYTQPMKRTV SDNSLSNSRG EGKPDLEFGG KSKGKLWPF I KKNKLMSLLT180
GGPFSE 186

(2) INFORMATION ON SEQ ID NO. 212:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

"04022500"

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ISGRRVSLNF VSEFSITEFC PCWCLGYRPD GPGSFPSCSG LEVSPLHFLK ACVQCSPKSI60

(2) INFORMATION ON SEQ ID NO. 213:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 68 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

DLCSTLSATK GSITCFLNKA LVSPPASSGL HYSETNSTSF AGGITVPISR LGPALQTSFG60
LLVLLTLL 68

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 54 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TISFFKSKRG LKQEGTGTSS QMDLGEHCTQ ALRKCKGLTS RPEQDGKLPG PSGL

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
LPTAFLLSSV FWIFMTWFIL FFPDLGAPF YFSFIFSIVA FLYFFYKTWA TDPGETKASE 60
EEKKVNIIITL AETGSLDFRT FCTSCILIRK LRLSLHCHVCN CCVARYDQHC LWTGRCIGFG120
NHHYYIFFLF FLSMVCGWII YGSFIYLSH CATTFKEDGL WTYLNQIVAC SPWVLYILML180
ATFHFSWSTF LLLNQLFQIA FLGLTSHERI SLQKQSKHMK QTLRLRKTPT NLGFMQNLAD240
FFQCGCFGLV KPCVVDWTSQ YTMVFHPARE KVLRSV                               276
```

(2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```
SPSRSPVVFA GEFLFKHPFV EESLMSFFHP DLHLMNPKAI STQFLYSVF
```

49

(2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

KEINNYIRKE KNFKYLQPST PNHPQDRWVQ KNAPWFY

37

(2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KFSSKDDRTS RRRSIIISER KKILSIYNPL LLITPKIGGS RKMHLGFTEE RS

52

(2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

DKRNGIISKK LSPEKTTLKS ILKRKGTSDI SDESDDIEIS SKSRVRKRAS SLRFKRIKET 60
 KKELHNSPKT MNKTNQVYAA NEDHNSQFID DYSSSDESLS VSHFSFSKQS HRPRTIRDRT120
 SFSSKLPSHN KKNSTFIPRK PMKCSNEESC 150

(2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

NKWNKSKLGK EISKATQSLD PAQLADPCHS LAVAASLCSL KGEPGQCFPS PWAWSLHSGK60
 QTSGPFPKSQ ECLAAWVLI AMF 83

(2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

NSKLVDCRME TWLLRHWVSF SLCVSCWGVV MIVSALTHCT RWQQDTALHK MAAPLQLPPQ60
 PPSLHPHRFG LWFLSSVTYC LRS 83

(2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CLHNREPDIF RILSSSYGI LRPRSYLQTK WPWSLQNIAM STHQAARHSW DLGKGPLVCF60
PLCSDQAQGL GKHWPSPFS EHREAATARE 90

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

QSLRHCWLN I SLQRDGA FKE PGAGPVSSKA LDVFLVRTRR GCQMPLKPSG LVWPRAAGQG 60
RAEKWSSSQL ALPSPTQPRP RWSLDSILTS ASPKVQMSKC LVVQSQEMGS YLKS 114

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 145 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GCVGGGRAEA MAEKFDHLEE HLEKFVENIR QLGIIVSDFQ PSSQAGLNQK LNFIVTGLQD 60
IDKCRQQLHD ITVPLEVFY IDQGRNPQLY TKECLERALA KNEQVKGKID TMKKFKSLLI120
QELSKVPED MAKYRSIRGE DHPPS 145

"BIBL" 0407/95B

(2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GQTMRTTEGLR GVSRAQSHLS RKVASALAVP ASRRIAVPGD LHTGRVSWLR RRVILPPDAS60
ILSHVFRKYF RKFLNQAFK FLHGVDLAFN LLIFS 95

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ALRPPLYALG QQVGAVTGPA DCSATAPLDF WIEWKQSQNS GLLGGWQRGM VRGPPFISLF60
SIRWQSTGHP WWVSGPRPMP TLPFESR 87

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

APALATQPPL SLPRGTGPAY LNSLTMLQT WLLDSKLLSS NVLLPHFHFL HICLLLYWFL60
LLNLYFHSWV LCLPPFFSA 79

(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

RSMSVEASFV CLGTTGRCCH WSCRLEFSNP FGFLDILETK SEQWPTGGLA EGYGKRTSFH60
LPVQHMAVH RSSLVGVRPK THAHLTL 87

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATLSRFFGRI FNLRLTQVFP FLSSPNDKK SFCSEGEWN GVMYAKYATG ENTVFVDTKK 60
LPIIKKKVRK LEDQNEYESR SLWKDVTFNL KIRDIDAATE AKHRLEERQR AEARERKEKE120
IQWETRLFHE DGEWCWYDEP LLKRLGAAKH 150

"DDE" 4353

(2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

DSLRRGLGIC LWEFIHLSLL FTSPKPGFPL LKPAVISQLE GGSELGGSSP LAAGTGLQGS 60
 QTDIQTNDL TKEMYEGKEN VSFELQRDFS QETDFSEASL LEKQQEVHSA GNIKKEKSNT120
 IDGTVKDETS PVEECFFSQS SNSYQCHTIT GEQPSGCTGL GKSISFDTKL VKHEIINSEE180
 RPFKCEELVE PFRCDSQLIQ PSREQH 206

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

RIRRSALIFS KGVQRWRRVF GRRVSPGSGN TESEASDYRK KQGTSKVFGR RVLKKIQ 57

(2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

GTLFFTVVTG FALCVPAAGT YPPSENPPPS LYTLGKDQCR TPDF

44

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 74 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

NLYPTLEFNP SHFVVELTGF FSTPFFRTPL RYLVEYGS HW LRS LC SRCRD LPAFRKPAAI60
SVHPWKRSVQ NAGS

74

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 183 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AAVAFGAKGT SPAEARSSRG IEEAGPRAHG RAGREPERRR SRQRRGGLQ ARRSTLLKTC 60
ARARATAPGA MKMVAPWTRF YSNSCCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP120
DQYNFSSSEL GGDFFEMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAG SSHSSVTRSL180
TLP

183

"SECRET" 040495B

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

CQHVVHCHCDF SSHDPDMCYG YLRVQATRS WIIPFFCYQI FDFALNMLVA ITVLIYPNSI 60
 QEYIRQLPPN FPYRDDVMSV NPTCLVLIIL LFISIILTFK GYLISCVWNC YRYINGRNSS120
 DVLVYVTSND TTVLLPPYDD ATVNGAAKEP PPPYVSA 157

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

ATKTVPRQRW SPPHCPRPNP SLNLLRCGWG NRGKTEAPDA FSLLCSSAID CPDVQRETH60
 RFAHENWGAD GQADRLCLFS E 81

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GVDGETEAKL RHLMHSACCA AVPLTALMFR EKRTQGLPMR IGEQMAKQIG YVCFLSDEV60
KPCGSGGHLW FILFPYPWLL EMVTFRTVQL HLSEHYC 97

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

LEILGIFSRV SKLSSSPTDT HPSSQIGVAI LGGRVVYGTP GCLHISQNYR RTIVPKSRVF 60
TGRQNLFSMP VPQLLSQIPV LGSHQLPIPH QTATVPSLSP YCSFKSCSQE RNCH 114

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 53 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

IPSPQGPFCR SYSDPRKCPF PIVVLCLWGL VYPRGNCGEI IGLRVKRALV LEL

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

QVDTLISTRK GLKLQNQC SL DSQTNDSTV TPGID

35

(2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TKPQRHRTTM GKGHFLGSEY DLQNGPCGL IYPYAVPWSN A

41

(2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```
GSVKVPASPR PGGTSLGPGV AAKELSFSPR NGRRGQLPRP PGSLTLLLFF SSPASRGPAS 60
LSPGGIRLLL PPPHLLPGQ PACPAAVMCD KEFMWALKNG DLDEVKDYVA KGEDVNRTLE120
GGRKPLHYAA DCGQLEILEF LLLKGADINA PDKHHITPLL SAVYEGHVSC VKLLLSKGAD180
KTVKGPDLT AFEATDNQAI KALLQ 205
```

(2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
RNMSSFSRAP QQWATFARIW YLLDGKMOPP GKLAAMASIR LQGLHKPVYH ALSDCGDHV 60
IMNTRHIAFS GNKWEQKVYS SHTGYPGGFR QVTAAQLHLR DPVAIVKLAI YGMLPKNLHR120
RTMMERLHLF PDEYIPEDIL KNLVEELPQP RKIPKRLDEY TQEEIDAFPR LWTTPEDYRL180
```

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
VIGYPSRINS EPSPIYNRP GNNVKLNCMA MGISKADITW ELTDKSHLKA GVQARLYGNR60
FLQPQGSMTS SACHKEGW 78
```


(2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATPLCGMLNG SLIPGVVEIC FHTDEPEPLP SDATYPLTPT

40

(2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

VGIWQEDHLP QSLGFLNKKE IVFLSWLLRL LKLALPLKYD ISFAVLNLKL VASSVAHFQF 60
 LYQASLLSFP LRMGQVCSGG HSVRFSRGFG RGFKGKYS GG RMGSGVKVGD KGGRAKGGVE120
 GWGPYLD RGM PGGQ GK 136

(2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

LVYPKQGTKE PGKRSGHVVR DTQDTLRDQS GSTPVLLEPC LCVNPFCLQN KRQQRKLLNQ60
NTDPMRNGAC FCDPGELSR LQELTDGQLL IF 92

(2) INFORMATION ON SEQ ID NO. 269:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

NLVYTMWLQI YVNVHFEHIY VLWKEMLVTK IRFTLKEEEF YSKHSNILEK CFKIQSIVFK 60
 VAVKASTYVK TQKEGSSDKN TAPLLCCFSC SLYTLSKHLL SGA 103

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

FIYQSKVRD IFAVTLAILS LQSPTSRVQC TSNNSLKTRH LTISVYLVCK VNKKSSIIKE60
LCFYQRSLPS EFLHKLMPSL QL 82

(2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

QQHHL PQSLG FLNKK EVVFL TWLLR LLKLA LPLKY DISFA VLNLK LVASS VPHFQ FLYQA60
 SLLSF PIRMD MCCSACHVCN ASCREFGHSI KEKIQ 95

(2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

LLHQYHTSSF YTKPVSSVFP LEWTC AVQRV MSVMLHAESL VIVLKRKYSE VTMSPE 56

(2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

HAEQHMSILM GKLRLRLAWYR NWKCGTDEAT NFKERTAKLM SYFKGRANFN NLNNQVKNTT60
SFLLRNPND 69

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

YILEISPLKP SLAPTSCGLM PQGFPPHFCN PRYPSLSTPS QTPTPGIARE DFGLANCVGY60
VSVVLIRDVH DCQSAFLTSTV TLLRCNSSQ KKTFS 95

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 133 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PTQFARPKSS RAIPGVGVWD GVDNEGVLGL QKWGGNPWGI SPQEVGASDG FRGDISNIYQ 60
PWALSPCCSQ HGPHTSSLRL TWELVRNAGS PRSIELEAVL TRSPVIFMAQ SSFLRDRCL120
LSAGMRHPWG RCG 133

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(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LKQHSNQHNN LLGQSLHGQS LGWESGMGWI MKDTWGCRSG VGIPGASVHR RWGPAMASGV 60
 IFPIYISPGH SRPAAHSMVL TPAASALPGS LLEMQDLPLD LS 102

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

VYSANEGQNF QFIDGYSAAD ESLCVSHFNF CKQRHRPRTV RGRTSFSSKL PRHNKENSTF60
 ISRKPMECNSN EEVVNQGGSD GSMGKF 86

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GAELVFLQNC LGIIRKIALL FQGNRWNVQM RKLLIKSRM DQWVNFRWRQ GGAYIHSNPD60
VIWSGQGWK 69

(2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

LTSSFEHSI GFLEIKVLFS LLCLGNFEK LVLPLTVLGL CLCLQKLKWL THKLSSAAE 59

(2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GKEPQPESNS IMVKFPTSS CEWVIRKNEK PKDKNQRQMG SVTGLSSIL NPIEYCGLTK60
CQGGD 65

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(2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

FLSFGSSFFL ITHSQDDSVG NLTMIELLSG WGSFPHRKDI LKTKKYLN

48

(2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ARNIQSDLEW MIKIQSQTPS VFDFCLLDPH FS

32

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CAKLETGFDF LSYLFAFCAS PSNLVHLSSH SCYFQVKQDI LGVKSLWVFC FYVYKNGFCV60
PFPCYQLIW KLTIIM 76

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 63 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

VELSLLFPQL SQLLVNFKEA GHDDSHLLSQ NFGRRRWADS LSPGVQDEPG QYGPTSSLTK60
HPH 63

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 73 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

PPKCLVSLEN NMNETKDEPD YLVTHRRRTS SSGNQILFQA WHIKGKKGSE RRVRYHLKP60
QKIWQKTASK SIR 73

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(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

PLGPASSAFG PSGSKSRSEE GRDGTASPGT FKYHPWSPLS SLREWTSQST SSGLSDLLLC 60
 LYQPWQGSRI HLVGSGPSQY HWGSNKFLEP QSLGPGSQLI GDGVPFQARA EFGTSGHELE120
 GNSVSYELGP WP 132

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

ESRRGALAGP LSKAGEGRPG WYLNVPGLMS HPFLPHSYSL TLMAKARDAG PKGKNVLSVF60
 SGFYSLVSLH 70

(2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

GVKAREYRED VFTFRACVSG FGHQQRVGV RKEGMGQHPW DVQVPSWSPF SSLREWTSQS 60
TSSGLSDLLL CLYQPWQGSR IHLVGSGPSQ YHWGSNKFLE PQSLGPGSQL IADGVPFKLV120
PARAEFGTSL KGNSVTYELG PWP 143

(2) INFORMATION ON SEQ ID NO. 304:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 408 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

FANWEFMGTE QLQPQLPSPK VWSCRGCRQG PTKFNQVSRM QTPAPVSRRV GLAVSLTPPP 60
SGQSGPSVMG KAAACPATPA SAPSQGLSFG GPVSCWPGSP LLHLIGGRQL LDLCPGCGRS120
LPFSSSSSSS VSNDAPDGP RGLGCFGGVV LGGRGFKYLL YFLFVAATQQ ILLGRASAF180
LKRDVGDPLV VAPAFFAVAG HLHQAVALPG VVRVRDQET MQVSGLGAL GLGRLSQELR240
QALHARHPHD VDVVVTAEGL DEREVDLQGD VILLLLVNGQ EAEDHAVVWH IHQLGRLVHP300
HCEAILALSG HQKLLHRGGH RLHLLRRVVA RHELFQRHVA IIIHSGCGST AVPREKLQNP360
SQRAQNLPTL LERSSKTFGK QRNPSRKGGK IYCKVLGEDN PGSCGNQR 408

(2) INFORMATION ON SEQ ID NO. 305:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 169 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GWGVWQAGLD PVLGPPSSAV PSLLLGVVSM VWPHLQLCLS AVPLASSSLN SAAWSPVSSR 60
ARQGWGGWCW QQLLSWCDLS GLHLRGRNGP GYRGQIHPCW SPRPPGLGAA GGRWLLVGRW120
PSCLACLPCL SSSPNALSVS AFLAPGLSTP SAYKAVSPPQ TTVWLQPIR 169

(2) INFORMATION ON SEQ ID NO. 306:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 120 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ILQLGHQFPL VPARAGAVGV GSSFSLGATF PASTSEVGMG QAIEVRFIQA GVLVLRAWGL 60
LGGAGCWWEH GHRAWLVFPA SLLLLTLCLS LLSWPRASPL PQLIRLCLLL RPQSGSSPSG120

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 472 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

SESLTHPGEE PGGPPPGGAP TMAPLVAGP AALRFAAAAS WQVVRGRCVE HFPRVLEFLR 60
 SLRAVAPGLV RYRHHHERLCM GLKAKVVVEL ILQGRPWAQV LKALNHHFPE SGPIVRDPKA120
 TKQDLRKILE AQETFYQQVK QLSEAPVDLA SKLQELEQEY GEPFLAAMEK LLFEYLCQLE180
 KALPTPQAQQ LQDVLSWMQP GVSITSSLAW ROYGVDMGWL LPECSVTDSV NLAEPMEQNP240
 PQQORLALHN PLPKAKPGTH LPQGPSSRTH PEPLAGRHFN LAPLGRRRVQ SQWASTRGGH300
 KERPTVMLFP FRNLGSPTQV ISKPESKEEH AIYTADLAMG TRAASTGKSK SPCQTLGGRA360
 LKENPVDLPA TEQKENCLDC YMDPLRLSL PPRARKPVCP PSLCSSVITI GDLVLDSDEE420
 ENGQGEKES LENYQKTKFD TLIPTLCEYL PPSGHGAIPV SSCDCRDSSR PL 472

(2) INFORMATION ON SEQ ID NO. 308:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 138 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

PGFALRGAIG PREGRGGGRG YRRSSGRQPL VSWQRQARCG SGGAMSFCSF FGGEVFQNHF 60
 EPGVYVCAKC GYELFSSRSK YAHSSPWPAF TETIHADSVK KRPEHNRSEA LKVSCGKCGN120
 GLGHEFLNDG PKPGQSRF 138

(2) INFORMATION ON SEQ ID NO. 309:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 121 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

SYGATAAFLS RSEASYFRD CETGFRFLPS WTRGQGCAPS ACLPSRSQTI PTLAGLEGFD 60
 QSGSCSDQGG GGWQGRPPFP FCLLSSLGDV GLSFGEDESL SWNWASQGRV QRQGQEKKVR120
 V 121

(2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 249 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SEQGAKSADS VAAQPRPVPA EGMNHQQMSL FSKKRKGLVQ SRGLGSVLMF QPLRPAFLSR 64
 RPGFQLQGGM ANVWPQCGGR LGVWVAARLV TLGGRSFFAF RDKLQRAAEY SESGLPRLGA120
 VVQELVAQPI ATLATGHLQG FRSLVLRITLG HAVGVNGLGE RRPWRRVCIL RAAGEQLIAT180
 LGTHVNAREK VILENLAPPE AAERHGATGT AARLPLPTDQ RLPTRRPPVP ASTSPPLPRT240
 NRSPEGESR 249

(2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 204 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

LGSSWIFVNL TVRFCILGKE SFYDTFHTVA DMMYFCQMLA VVETINAAIG VTTSPVLPSL 60

IQLLGRNFIL FIIFGTMEEM QNKAVVFFVF YLWSAIEIFR YSFYMLTCID MDWKVLTWLR120
 YTLWIPLYPL GCLAEAVSVI QSIPIFNETG RFSFTLPYPV KIKVRFSEFL QIYLMIFLG180
 LYINFRHLYK QRRRRYGQKK KKIH 204

(2) INFORMATION ON SEQ ID NO. 312:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 155 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

RISGCSPRSS CCFQCPTADR FKKPTEQQQN EVFLRSIQKC TVPPLTRTST QVNGLSQCRR 60
WKAAIFYVCA QPYSLEVCLA YSNISLSKA VHCYCQFDLH TVFPLDPCYH LDLVCVCVYV120
CLCVCGLVWF ETGSCTVTPG CSAVAQSRLT AALTS 155

(2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 70 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AVMDQVMQFV EPSRQFVKDS IRLVKRCTKP DRKEFQKIAM ATAIGFAIMG FIGFFVKLIH60
IPINNIIVGG 70

(2) INFORMATION ON SEQ ID NO. 314:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 112 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

FRNRKHLERK KKNPQNIQAN LYSVSFSPHP TCSPISKMK N SLPKCIQPPT MMLLIGIWIN 60
 FTKKPMNP II ANPIAVAMAI FWNSFLSGLV HLLTSRMESF TNCRLGSTNC IT 112

(2) INFORMATION ON SEQ ID NO. 315:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 110 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

DEKLSSKMYS ATNNDVINRN MDQFHKEANE SHYSKSYCCC HGNLLEFFSI RFSASFNQPN 60
 GVLYKLPTWL NKLHYLIHDC LPNRHLKCQG HVALELADGG PPEPESGFLP 110

(2) INFORMATION ON SEQ ID NO. 316:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

GSSEGSYSSQ TETCPLTPSL VTGSMFAQNF LRGLSLQKSN LLPECCLASE NLTLSFPSVN 60
 GHRCAVQGE TSESRAQWHG VALVVRKVIG QLYCKRNKYV VQFCKCQVCS VVL 113

(2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

GKRGQLWSLN LLAPCAGYKT RSWSKIALTP NPNAVQDLGA TQPVVIWCWF PFFVCLLVSK 60
IALLGTAWKV QAFLLARSL ASSPCLHSVP KEDFCSTLWS 100

(2) INFORMATION ON SEQ ID NO. 318:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

SQIISNLVDN YSIQELMFSE TVINRIFTSG LAGRLGGRKG RVEGWVAHQN GDEPGKTTML 60
LFLYPLKPIS RVLNDAFFVC FLIGSQISFS IKNWGYKPKE T 101

(2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

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WWRLNNKSAK VRQQAADLIS RTAVVMKTCQ EEKLMGHLGV VLYEYLGEY PEVLGSILGA 60
LKAIVNVIGM HKMTPPIKDL LPRLTPILKN RHEKVQENCI DLVGRIADRG AEYVSAREWM120
RICFELLELL KAHKKAIRRA TVNTFGYIAK AIGPHDVLAT LLNNLKVQER QNRVCTTVAI180
AIVAETCSPF TVLPALMNEY RVPELNVQNG VLKSLSFLE YIGEMGKDYI YAVTPLLEDA240
LMDRDLVHRQ TASAVVQHMS LGVYGFGCED SLNHLLNYVW PNVFETSPHV IQAVMGALEG300
LRVAIGPCRM LQYCLQGLFH PARKVRDVYW KIYNSIYIGS QDALIAHYPR IYNDDKNHLI360
IRLMNLGL
368

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(2) INFORMATION ON SEQ ID NO. 320:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 121 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

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YPFFFTLCQRN RVFDISSYVK EMLQNVNCFK LKLPLKRPRY IYLIVYIMFN ICQSILQVCS 60
FISIKYGYV AQLLKWYICV YICTPNNIVC TFCFLYCICA GFFRLYQC�L CLLRYVQKMS120
I
121

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(2) INFORMATION ON SEQ ID NO. 321:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 114 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

FFFFFFFF HSNVYFFFFFF FFFFFGKNVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60
YYKYNIQFKK TYGETQLMFF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 597 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

EKCGQYIQKG YSKLKIYNCE LENVAEFEGE TDFSDFKLY RGKSDENEDP SVVGEFKGSF 60
RIYPLEDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQPQDNNGLC DPYIKITLGK120
KVIEDRDHYI PNTLNPVFGF MYELSCYLPQ EKDLKISVYD YDTFTRDEKV GETIIDLENR180
FLSRFGSHCG IPEEYCVSGV NTWRDQLRPT QLLQNVARFK GFPQPILSED GSRIRYGGRD240
YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGKLMWV300
DVFPKSLGPP GPFENITPRK AKKYILRVII WNTKDVILDE KSITGEEMSD IYVKGWIPGN360
EENKQKTDVH YRSLDGEFNE NWRVFVFPDY LPAEQLCIVA KKEHFWSIDQ TEFRIIPRLI420
IQIWDNDKFS LDDYLGFELE DLRHTIIPAK SPEKCRDMI PDLKAMNPLK AKTASLFEQK480
SMKGWVPCYA EKDGARVMAG KVENTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540
SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLLFVAVL LYSLPNYLSM KIVKPNV 597

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

76

(A) LENGTH: 42 amino acids

- IRNEKKGCVL SVGEMELVLV VLEQDRHLVL MLWSFVIVEH RG

42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

ATCSDNRSKI FOLFMLECYV LLEPAICMYR INNFYSFGQV ILRQSOWIQK

504

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

PKGVVVNPGA LLSQRTTASE LSACPAPTLP GPVPSHLLIR HSLSSHSL

48

(2) INFORMATION ON SEQ ID NO. 329:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 100 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ISEVAVNFSV LLLASVCLPI DTHYTNVPSK CSLHICFHCV PTGAMKCVRS PSSGGMSAAL 60
TTAIRIVLCG IFIYINFICT VISLFICQVT ICKSYTHKLL 100

(2) INFORMATION ON SEQ ID NO. 330:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 122 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENAAAD SLFQRRSFER RVCYISFFTV 60
TLWRLKDLVV SCFLKITGIW RPVKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFDPDYIV120
LS 122

(2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

ENWASRYFQS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKycwIKAI 60
 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFFLQ DLAVTQDGVQ120
 WHDH 124

(2) INFORMATION ON SEQ ID NO. 332:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LNVDLLITRR LCEKIYVYIY MICRSHFFYQ ALFSLQSHSL TVCNSWFMLM IDKYPVFEVTF60
 SNYHCNDNLS HVYTCNFLAS FP 82

(2) INFORMATION ON SEQ ID NO. 333:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

RLVKYKNSLN REKASQVFPL KVKYGTFFHN KVNDKFLTF FRRKKKTSYE PSLVNHLVYK60
IFPLEKKKFC KILRSHEIMP WS 82

(2) INFORMATION ON SEQ ID NO. 334:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

KLEYIMSTAN CSFCLILTDY AFPQRSSRSY IYRHIYGSGL KEKTLSSIM IYHCAINQKN60
QVRNTIKTTL KGKNF 75

(2) INFORMATION ON SEQ ID NO. 335:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

NEYCSWSTCI KQKTCQLLGA NTQNLVPVFF FELTTIVYTF LKIKFVTKSP MSFTCIYDHQ60
MVIRATYVNA CL 72

(2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

THNTSTITAY RKLQSTLQAS KVHSAQSPW RGRDLKVLMS SYFTCFLLST QCKMNFHSL60
YFRLKIDSFL VLTLTLEGT VPGKRSRFTV PNH 93

(2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

LGPRGEIEVY LAKSLAEKLY LCQYPVRPAS MTYDDIPHLS AKIKPKQQKV ELEMAIDTLN60
PNYCRSKGEQ IALNVDGACA DETSTYSSKL MDKQTFCSS 99

(2) INFORMATION ON SEQ ID NO. 338:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GKSRRSACPS ASRNTCWSRR RRRPRPSAQS APLCCGNSWG SGCWPSQAL PSAAWA 56

(2) INFORMATION ON SEQ ID NO. 339:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 59 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

GRAEGLLVHQ LRGIRAGLVG AGPVHVQRNL LPFAAAIVGV QGVDGHLKLY LLLLGLDLG 59

(2) INFORMATION ON SEQ ID NO. 340:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 157 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

QPSSLLHHCP YPYPPRHLLA TPLLKPQLLA GSPAHLIS FLASPQRASR QHGGPSQRAG 60
TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPA GDRRPLPEWG RVSLAESPGA120
EFRCPGSLGE WGEIPEKESS AHPKTEEAAL CPAGSH 157

(2) INFORMATION ON SEQ ID NO. 341:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 260 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

NHSCWQGPQL MPASSPFLLA PKGPPGNMGG PVREPALSLVA LWLSWGAALG AVACAMALLT 60
 QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQK120
 QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA QGYGVRIQDA GVYLLYSQVL180
 FQDVTFTMGQ VVSREGQGRQ ETLFR CIRSM PSHPDRA YNS CYSAGVFHLH QGDILSVIIP240
 RARAKLNLSP HGTF LGFVKL 260

(2) INFORMATION ON SEQ ID NO. 342:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 201 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESSLEVALM GTRCRTECCF FCFWVSTALL 60
 FRDLSPLSQA SRASELCGR LCQGYPSFPW EGPPVPCSLR TSLRLCSSV CWVSRAMAQA120
 TAPRAAPQLN QRATESAGSL TGPPMLPGGP LGASKKGDEA GMSWGPCQQL WFQEWGSKEV180
 AGRVRVRAVV QKGRLLRKE K 204

(2) INFORMATION ON SEQ ID NO. 343:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 165 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GRRSRMEIPV PVQPSWLRRA SAPLPGLSAP GRLFDQRFGE GLLEAELAAL CPTTLAPYYL 60
RAPSVLPVA QVPTDPGHFS VLLDVKHFSF EEIIVKVVGE HVEVHARHEE RPDEHGFVAR120
EFHRRYRLPP GVDPAAVTSA LSPEGVLSIQ AAPASQAAPP PAAAK 165

(2) INFORMATION ON SEQ ID NO. 344:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 116 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TALAQPOASQ AQSPHPPNVL DCTDLPLQTI QAWFPRPDPS PATRQSTTAP SSPFSAVKPQ 60
PATPDSGTLF RLPQLLDTRP TRTPNTKLYR LSHPNLPRLC TDVLGPLPNS NQTPSP 116

(2) INFORMATION ON SEQ ID NO. 345:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 111 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

DIRAESGEVG VGESVQFGVG CSSWPGVQEL GQSKKGSRVW CGWLGFHGRK WAGGGSCRLS 60
GCRGRIGSWE PGLDGLEWEV CAVQDVWVG GLCLTGLGLG QGCLHHLNLS K 111

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 53 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

RTEEEKKKKKE KNQQPQLPTP KCWSFYVKGR IPGYGHGVYK YVGRFSANSF PTV 53

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 51 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

NELKWTNRAE LSVGWQSWKP AFPASHQLNE VMSIQLRLF FKNNHAFLNP N 51

(2) INFORMATION ON SEQ ID NO. 348:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFVL VLALFLIFFY 60
 YESPGRRGDS GSWPGPGRQV ALEMGKCLCR GAELSLCFSE FPLLLPLHTP VAGRNLGFPE120
 SLGVPPFLPH PGGTPRAPGL FLLLFSEWAV 150

(2) INFORMATION ON SEQ ID NO. 349:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

RSFLTRSVIK LPKRKTRGET SPGPWAFPLG GVRRVGPPSF QGSRGSFQPR GCEGEGVEEK 60
 RRNRERAQRL DTDTFSPGP PAVLAQASSH CHLCVQEIHN KKKSKTKPKP KQNPKGKDLG120
 QWNEEEGRRG R 131

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

RKKGETEREL SASTQTLSHL QGHLPSWFRP APTVTSASRR FLIKKNQKQS QNQNKIQKEK 60
TWGNGMRKRG GEEGRAGLW MHNSRARGLG RKIPQRPAAAC VALARHVVFV GRLPIHPVEI120
LVAGLLGGVK PVSDRQAGKG LGDGGCGRER V 151

(2) INFORMATION ON SEQ ID NO. 351:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 108 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

TLTAHEGRGG KCTEEDASQ QEGCTLGSDP ICLSESQVSE EQEEMGGQSS AAQATASVNA 60
EEIKVARIHE CQWVVEDAPN PDVLLSHKDD VKEGEGGQES FPPELPSEE 108

(2) INFORMATION ON SEQ ID NO. 352:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 77 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

KFFGNSLHAT PKCTPITLWL FSEKDFSQIV PFTPLRAALG NSPDHLLPPS RHLCVTAGHP60
GLEHPPPTD THEYGLP 77

(2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 122 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TYSIHLHSQT KLKSLKVHKK IAQLKSAEYT QNCHPTVFSV FPAILFPPQT SSAPSHPKYA 60
 IVFVILIKIL KQKFIVEQFM STKVCLSCSC PVCISSGFII QIKKILKNFL VTACMQPLSV120
 PL 122

(2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 457 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

PVCEPLSCGS PPSVANAVAT GEAHTYESEV KLRCLGYTM DTDTDFTFCQ KDGRWFPERI 60
 SCSPKKCPLP ENITHILVHG DDFSUNRQVS VSCEGYTTFE GVNISVCQLD GTWEPPFSDE120
 SCSPVSCGKP ESPEHGFVVG SKYTFESTII YQCEPGYELE GNRERVQEN RQWSGGVAIC180
 KETRCETPLE FLNGKADIEN RTTGPNVVYS CNRGYSLEGP SEAHCTENGT WSHPVPLCKP240
 NPCPVPFVIP ENALLSEKEF YVDQNVSIKC REGFLQGHG IITCNPDETW QTSAKCEKI300
 SCGPPAHVEN AIARGVHYQY GDMITYSCYS GYMLEGFLRS VCLENGTWTS PPICRAVCRF360
 PCQNGGICQR PNACSCPEGW MGRLCCEPIC ILPCLNGGRC VAPYQCDCPP GWTGSRCHTA420
 VCQSPCLNGG KCVRPNRCHC LSSWTGHNCS RKRRRTGF 457

(2) INFORMATION ON SEQ ID NO. 355:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 210 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```
GVRAASKEIE ELRRAHREGT SRAVTGEGPA AGRMTVPKQT QTPDLLPEAL EAQVLPRFQP 60
RVLQVQAQVQ SQTQPRIPST DTQVQPKLQK QAQTQTSPEH LVLQOKQVQP QLQQEAEPPQK120
QVQPQVQPQA HSQGPQVQL QQEAEPLKQV QPQVQPAHF TAPRAGAAAA EEAGPDTDFS180
TGAHTGHSQA SRHRELLPGA VFSFRPPGAG 210
```

(2) INFORMATION ON SEQ ID NO. 356:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 292 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```
GRAGRATMF SQQQQQQLQQ QQQQLQQQLQQ QQLQQQQQLQQ QQLLQLQQLL QQSPPQARCH 60
GVSGGPPQQP QQPLLNLQGT NSASLLNGSM RQRALLLQQL QGLDQFAMPP ATYDTAGLTM120
PTATLGNLRG YGMASPGGLAA PSLTPPQLAT PNLQQFFPQA TRQSLLGPPP VGVPMNPSQF180
NLSGRNPQKQ ARTSSSTTPN RKDSSSQTMP VEDKSDPPEG SEEAAEPRMD TPEDQDLPPC240
PEDIAKEKRT PAPEPEPCEA SELPAKRLRS SEEPTEKEPP GQLQVKAQPQ AG 292
```

(2) INFORMATION ON SEQ ID NO. 357:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 169 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

```
PRRLPSVAVG MVRPAVSIVA GGIANWSSPC NCCKSKALCR MEPLRREAEL VPWRFRSGCC 60
GCCGGPPLTP WQRACGGDCW SSCWSCSNCC CCNCCWSCC CCNCWSCCCC CWSCCCCCW120
NMVARLPARP QRSSRPHGWA GPAAPTPRPG GSGPRAPGLP AATPGPVGS 169
```

(2) INFORMATION ON SEQ ID NO. 358:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 158 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```
ISKTKKYCGS PSSRIRLEGG HLEMRKARGG DHVPVSHEQP RGGEDAAAE PRQRPEPELG 60
LKRAVPGGQR PDNAKPNRDL KLQAGSDLRR RRRDLGPHAE GQLAPRDGVI IGLNPLPDVQ120
VNDLRGALDA QLRQAAGGAL QVVHSRQLRQ APGPPEES 158
```

(2) INFORMATION ON SEQ ID NO. 359:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 119 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```
QSLRTLNLKN KKVWISLEP NSARGRSPGD EKGPRGGPCA CVPRAAERRG GRCCPGAQAE 60
ARARAGAOTS CPGGPEAGQC QAQPGPETAG WLRPEATAG PWPSCRGSAG PEGWGHHP 119
```

(2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 187 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

PPEFGWDAAE TDLLLAEEGS GWRGPHGQOV LGLLWRPRL SKLPAVDHLQ SSPRSLAELG 60
 IQGATEVVHL DIRQGVKAND DPIP RGQLTL CMRAKVPPSP PEVGASLQFQ VPVGLGIVRP120
 LAPRDSSFEP QLWLWPLPGL LGSSVLPASR LLVGHRHMPV PAGLSHLQVT ALEPNSARGR180
 STVLFCF 187

(2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 86 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

STIILGKSRI EFFSRCPTRV GQGPQSRLIN SHRIQTPGKI ALRSQLLSSL YGSRKNSTKM60
 TGHPM SVMPM KPHLLEKPLN QNYLFS 86

(2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 83 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

ITKAIVFSFV FSSGYTVEVR ESLILLFGAI IKAMQQPKIK HFGSSQDDMS GDRSCGSHSN60
NLMGPPEKTG VNVLSFYMQ ELC 83

(2) INFORMATION ON SEQ ID NO. 363:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

YKNDRSSYER HANETPSSGE ALESELSFFL MSSDAASFLI FLKTVCF CGM YICTPNYLAL 60
GNHSTTQRQL NKEKFNFKYQ VLSNISQTS D FIKGLPANKV HPKYTGEKAR LLQGPRV 117

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

SCRCFYCMPD MPLTREWRTD NSPRMTRRHS HVICIFSYQL QIVALLRLPP VQQEMERKHF60
SFLHTTPLDN WKYFWVITIL GYF 83

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(2) INFORMATION ON SEQ ID NO. 365:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

QYGPSRVEVE MSYRIANTLG SFLPRLAQSR QQQQNVEDAM KEMQKPLARY IDDEDLDRML 60
 REQEREGDPM ANFIKKNKAK ENKNKKVRPR YSGPAPPPNR FNIWPGYRWD GVDRSNGFEQ120
 KR FARLASKK AVEELAYKWS VEDM 144

(2) INFORMATION ON SEQ ID NO. 366:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

KPTKHRCCQH PKKYRYLNPN IRSRIFFCGQ NWHSTSCWSV WAPIISTDNC YHWISRCCLCP 60
 LPQPSHPHSL RKVTYPQHSI CRQVPFLPSC WQAWQSASVQ IHWICPLRPS DIQARY 116

(2) INFORMATION ON SEQ ID NO. 367:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

SSENPPNTAA VNTPRSTGTS IQTSGLEYSS VVKGTGIQOVA GLCGLQLLAQ TTVTTGYLAA 60
YAHYHSPATP TASGKLHILN TPFVGKFLHC LLAGKPGKAL LFKSIGSVHS VPAISRPDIK120
SVGRRCWTTV ARSHFFILVL LGLILLDEVG HRVFLSFLFS 160

(2) INFORMATION ON SEQ ID NO. 368:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 227 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

WESMNRWYVK PLETSSSKVK AKTIVMIPDS QKLLRCELES LKSQLQAQTK AFEFLNHSVT 60
MLEKESCLQQ IKIQQLEEV L SPTGRQGEKE EHKWGMEQGR QELYGALTQG LQGLEKTLRD120
SEEMQRARTT RCLQLLAQEI RDSKKFLWEE LELVREEVTF IYQKLQAQED EISENLVNIQ180
KMOKTQVKCR KILTKMKQQG HETAACPETE EIPQEPVAAG RMTSRRN 227

(2) INFORMATION ON SEQ ID NO. 369:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 155 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

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```
FIFSLEGSSG RAVPAAQAGG KGGALLLKGG WERSWSESES ESQEGSGGLR HWCPLWPLRL 60
EALGQAPEHK VRLSMEFCST CTADHISLSS FWRSSFQQPL APAVSLQSPD RRLSHDPAAS120
SWSGFCGISP AFSAFSECSF SSLRSHPPAL GASDR                                     155
```

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

DLILLRLELL IDEGHLLPHQ FQLLPQELLA VPDLLGQQLO AASGAGPLHL LTVTQGLLQP 60
LKALGQGPIQ LLPALLHAPL VLLLLSLAAC GAQHLEFKLLN LDLLQAALLL QHGH 114

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 201 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

TASTLRAVFP RPASESPPLR ARSDAEDLTA AMSSNECFKC GRSGHWAREC PTGGGRGRGM 60
RSRGRGFQFV SSSLPDICYR CGESGHLAKD CDLQEDACYN CGRGGHIKAD CKEPKREREQ120
CCYNCCKPGH LARDCDHADE QKCYSCGEFG HIQKDCTKVK CYRCGETGHV AINCSKTSEV180
NCYRCGESGH LARECTIEAT A 201

(2) INFORMATION ON SEQ ID NO. 372:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 189 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

LATAVTVDFT CLAAVDGYMT SFTTPIALHF GAVFLNVSEF STRIAFL LIC MVAVTSQMAW 60
 FATVVAALLS LSLGLLAVLG NVATSTAVIA GILLKITILG KMTRLTTAIT NIWKRRGNKL120
 ETSATASHST TTASTRTFP GPVARSSLE ALIAAHGCSQ IFRVGAGPQR RRLGRRPGED180
 GSQGRGCLF 189

(2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 316 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GGDPVVSSSY RSVGCSEQQK PASSDVVLP A TMSYTG FVQG SETT LQSTYS DTSAQPTCDY 60
 GYGTWNSGTN RGYEGYGYGY GYGQDNTTNY GYGMATSHSW EMPSSDTNAN TSASGSASAD120
 SVLSRINQRL DMVPHLETDM MQGGVYGSGG ERYDSYESCD SRAVL SERDL YRSGYDYSEL180
 DPOMEMAYEG QYDAYRDQFR MRGNDTFGPR AQGWARDARS GRPMAAGYGR MWEDPMGARG240
 QCMMSGASRLA LPLLBEHHPR VRHVPGACEV GAPSRAASRF GFRVWQWHEA DEGGLGRRGP300
 QPICEPRRRR ESRAAF 316

(2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 200 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

IPAALLTGSI RMPPCFLFFF LVRKSAVVFP FPVRPHLLHA IAKPENQNGK PPGKAPQPRM 60
 PLEHAVLGDD VLGEEGGQAE RHQTCTGPGP PWGLPTCAHS LRPLAGRSGH PGPSVPWDR120
 RCRCHACGTG RGRHRIGPHR PFPSQQQARC SHSLTGTGRA HSGRPSSRRT HKSHTFLHLS180
 RTRLLASCLS PNAAPYLSAG 200

(2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 218 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

STSHDCVPQA DAAAYSRTAD GETEARGGRG GADLPASPSP RPRLAPPWPV RSTRGARRRR 60
 TARGQAGSSS AMAAQLGKR VLSKLQSPSR ARGPGGSPGG LQKRHARVTV KYDRRELQRR120
 LDVEKWIDGR LEELYRGMEA DMPDEINIDE LLELESEEER SRKIQGLLKS CGKPVEDFIQ180
 ELLAKLQGLH RQGLRQPSH SHDGSLSPLQ DRARTAHP 218

(2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

NQLKLKQQAG SFSQEGCKGE NILSFLQGN HCPGVPASGR HNLSKVQGML ARKGGILDCC 60
 LLSEPSPTPQ PASWCLFSSK LSLPNLSSSE GKRESVPGFS RVGERTGKGT DI 112

(2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

VRPEHSLMVL SLDTPTSYLQ FSRRRASGTL GCKPNLGSMF ALNPNSQRRS ECIFHAAAAG60
 CWPRFCVFSQ PSEITSFLVA VTNSSWTTMK LIYFPI 96

(2) INFORMATION ON SEQ ID NO. 378:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

SNRLVASPKK DARVKTEFFPS FCREIIALVC QPVVGTTFQK FKGCWLEKEV FWIAASSQNP 60
LLPHSLPPGV FFPPNSLYLT SLHQKASGNL FRVSVEWEKG QAKAQIFRRE SSYFWPLHVP120
YSGIVGPDDW HSDSQLWFEW NIRGS 145

(2) INFORMATION ON SEQ ID NO. 379:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 429 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

RQFEITSISV DVWHILEFDY SRLPKQSIGQ FHEGDAYVVK WKFMVSTAVG SRQKGEHSVR 60
AAGKEKCVYF FWQGRHSTVS EKGTSALMTV ELDEERGAQV QVLQGKEPPC FLQCFQGGMV120
VHSGRREEEE ENVQSEWRLY CVRGEVPVEG NLLEVACHCS SLRSRTSMVV LNVNKALIYL180
WHGCKAQAHK KEVGRTAANK IKEQCPLAEG LHSSSKVTIH ECDEGSEPLG FWDALGRRDR240
KAYDCMLQDP GSFNFAPRLF ILSSSSGDFA ATEFVYPARA PSVVSSMPFL QEDLYSAPQP300
ALFLVDNHHE VYLWQGWPI ENKITGSARI RWASDRKSAM ETVLQYCKGK NLKKPAPKSY360
LIHAGLEPLT FTMFPPSWEH REDIAEITEM DTEVSNQITL VEDVLAKLCK TIYPLADLLA420
RPLPEGSIL 429

(2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 169 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

(2) INFORMATION ON SEQ ID NO. 381:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GIPSEWLGA FITLVYCDFA ATMQSCFQGT LFLDLVRS GP SDLLRVGLGF ASVPQVDEGL 60
VDVKHHHGSS GPQAATVTGH FQQIPFHGHL STHAVQPPLT LHIFFFLFPP PRVHHHPPEL120
TLQETGGLLS LENLDLGPPF LVQLHRHQRR RALLTHGGVP ALPEEVDALL FAGCPHRVLS180
LLATSHCRAH HELPLDHIGI PLMELPDALF GEPAIVEFQD VPDIHGNAGD LKLP 234

(2) INFORMATION ON SEQ ID NO. 382:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 81 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

RLFAPLRTSW AVVIPGARVA LCFYKIMTYV TCLHVCLLVE FLNSQLTNHR KYYFLSYGFW60
FTGLRGFSEY LWPOQHTQFP S 81

(2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

IVNRTTACTL FEVNLEWKAR DYTLFKIDIC GAHTIYEIVP SKKEKKKIRR SNLEQHCLIK60
A 61

(2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

PPDFFFLFFR GYYFIYCVSP TNVYFKKSIV PGLPFQIHLK ESTCSSPVYN LIEMRK 56

(2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

(2) INFORMATION ON SEQ ID NO. 386:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

(2) INFORMATION ON SEQ ID NO. 387:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

FCIHFECLHV KTQLIIYFNI KPISFEAKLI LLFYKSNQDS FFRMLKAQCL RFMLAALLAL60
LLPLNQVGLS SLRRHTLHYF LWLQRRHHSP RDTGFH 96

(2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 221 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```
FIMLNIIILIK FSSFSIRCAI LSSVCLNEAI TFAFLQVFL WNMDKYTMIR KLEGGHHHDVV 60
ACDFSPDGAL LATASYDTRV YIWDPHNGDI LMEFGHLFPP PTPIFAGGAN DRWVRSVSFS120
HDGLHVASLA DDKMVRFWRI DEDYPVQVAP LSNGLCCLAFS TDGSVLAAGT HDGSVYFWAT180
PRQVPSLQHL CRMSIRRVMP TQEVQELPIP SKLLEFLSYR I 221
```

(2) INFORMATION ON SEQ ID NO. 389:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```
KGGATCPESP QDRKRRGNLD MEKLYSENEG MASNQGKMN EEQPQDERKP EVTCTLEDKK 60
LENEGKTENK GKTGDEEMLK DKGKPESEGE AKEGKSEREG ESEMEEVERE GTRGRGSG 118
```

(2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

```

RFPYLGFPIS RPPPSLTLP SLTFLLPLP HSLAFLYPLT FPHLLFCPCF LSFPRFLTSC 60
LPEYKLLAF SRLVAVLHFP SFLGLKPLH FHC RVFPCRD FPSFSCPAGI LDRLLLLFSF120
AERWEQQTRR PGRSWTKN                                     138

```

(2) INFORMATION ON SEQ ID NO. 391:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3218 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

"BIBL" 0404959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GCGACCACGA GCTGGTGCAT CCATCAGTAC CCTTGCCGGA CTTTCCCTTA AAGAAGGAGA 60
 GGATCAGAAA GAGATAAAGA TTGAGCCAGC TCAGGCTGTG GATGAAGTGG AACCTCTACC 120
 TGAAGACTAT TATACAAGAC CAGTAAATTT AACAGAGGTA ACAACCCTTC AGCAGCGTCT 180
 GTTACAGCCT GACTTCCAGC CAGTCTGTGC TTCACAGCTC TATCCTCGCC ACAAACATCT 240
 TCTGATCAAA CGGTCCCTGC GCTGCCGTAA ATGTGAACAT AATTTGAGCA AGCCAGAATT 300
 TAACCCAACG TCAATCAAAAT TCAAAATCCA GCTGGTCGCT GTCAATTATA TTCCAGAAGT 360
 GAGAATCATG TCAATTCCCA ACCTTCGCTA CATGAAGGAG AGCCAGGTCC TCCTGACTCT 420
 TACAAATCCA GTTGAGAACC TCACCATGT GACTCTCTTC GAGTGTGAGG AGGGGGACCC 480
 TGATGATATC AACAGCACTG CTAAGGTGGT GGTGCCTCCC AAAGAGCTCG TTTTAGCTGG 540
 CAAGGATGCA GCAGCAGAGT ACGATGAGTT GGCAGAACCT CAAGACTTTC AGGACGATCC 600
 TGACATTATA GCCTTCAGAA AGGCCAACAA AGTGGGTATT TTCATCAAAG TTACACCACA 660

 GCGTGAGGAG GGTGAAGTGA CCGTGTGCTT CAAGATGAAG CATGATTTTA AAAACCTGGC 720
 AGCCCCCATT CGCCCCATTG AAGAAAGTGA CCAGGGAACA GAAGTCATCT GGCTCACCCA 780
 GCATGTGGAA CTTAGCTTGG GCCCACTTCT TCCTTAAAAG GTTCCACTGG AGGGCAGATC 840
 CCAAAGGACA GTATCACCGT AAACCTGCGT TAAAAATGTT AAGCTGCTGC TTCATTAGGC 900
 CTTGTTTTATA ACGATGTACC CATGCACTAC GGAATTCTAT TGCTAAGAAA GTGGGAGCAT 960
 AGGCAAGGCA TTGGGAACAC AGGGTAGCTG CTGTTGCTCT TGCTCTCACC CCTGTTGACA1020
 CCAGTAAGTC TGTGTCTCCC TCACTGAACC CTGCACGTTG AGTAACAGCA GCATAATTCC1080
 ATCCTAGGAA AGGGGATGGG TGTTCCCTGG AATGGCATTG TATTTACCAC CTGAGAAACT1140
 CTGTACTGTC TCTTGATCTG ATCTCACTAA GGATCACAAAT GTCACAGATG AAACCTTAAAT1200
 GATAACCCAA AGGTAGACCT GCTGTTAATG ATCCAGCATT GGTCACAATG TACCAACTGC1260
 TTTCTGCATT CCGTTAAATA TCATCTAACA GTCTAAAACA TATCCCTTCA TTGCCATAAT1320
 GGCTGCCATT TTGCCATAGA TTTCCATATA ACTGAAAAAC TGAATTGTCA CTTTATCTTT1380
 AGTATCATGA TGATTGGAAA AACCTGTGAA GTTGTAAAG CACTCTCATT TGCCCTCTTT1440
 TTCTAAGTGA ATACAGGACA CGTATTAGTT GTTCTTAANN NNNNNNNNNN NNNNNNNNNN1500
 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNCAAGGG GGTAGCAGAT1560
 TCCATTCGTT TTCAATATTG CCACAATACC CAGGGATTAA TGCTGCCACA GGGGGGCAAT1620
 CTTTATTTGT CTTACTTCCT ACCCCTTCCC TGTTCTGCCT CTTTAACTCA GTTAAGTTGT1680
 TCTGTTTGGG ACCTGGAAAA GAACCCAAAG AAAACCTGAG TGGACAGGTT CATTTCTGGA1740
 ATGCAGAAAA CATTTTAAAG GCTAGATTTT TAGAATATTC TCAACTAGCA TTCTTTCCAT1800
 TGATTTGAAG GGGAAATTAA CTATTATAAT CTCTTGAATC CAAAACCTGGA TATTAAGAAC1860
 TTTCCCCCTT ACTAAGTTTA AGACTTTTGT CATGTGGTGA GTCAAATAAG ACCATTTTGA1920
 TTGTAAACCA TAAAAAGTT CAGCAAGTAG CCCACAGTTC TGGCCTAACA GCAGACTTGC1980
 TGTTTTCACT TGGTATCCTG GAGTTGGGTG GCTAACCTTA ATTTCTATGA TGTTTTCTAA2040
 AATGAAACTT GATAAAGTAG ACCACCAGCT GCACCGTGTT TTCTGTAAAA GTATTGTTAG2100
 TAAGTGCCCA AGAGACTTGA GGAAAAATACA GATTTTTTGT TTACCTTGGT CTTGTTTTAA2160
 GTCTTAAAAA ATTAAAGATA ACATTATAAT GTAGAATACA GATGGGACAT AGTCCTTGTA2220
 AGCTTCCCTT GAAATGTTT TAAATATTTA GGAAGCTTTT AAAAGACACT AAATTGTACT2280
 CTAAAAGACA CTAAATTGTA CTAATTGTAC AAAGGTCAAG CCAATTTTAT GAAACAGTCC2340
 TACAGAGTAA TATATGTGAT GCAGTGTAAAG AAGGAAAATA CTCATCTCTA ACATTATGGT2400
 AATAACATTT AGCCTCTTAG GAGTTGGAGC AGGGGGATGG GTAATTACAG ATTTGCAGAC2460
 TATAGAAAGA GTTTCATTTT TTTGTGACCC CACAGAGTCT CAAATTTTTA TTTCCTACC2520
 TGCTAGAGCC TACTGTGAAA TCACTGCTCC ATATTTGCCA GTGGAGGAAA TGGGCATAGA2580
 GTAGAGAATA GCTTCATATG GTTTACACGT TTGCATAGAC TACACACATG TCATGCGTTT2640
 ATGGCAGGTA GCTGGTATTT ATCCCCAAAG TAATAATGTT GAAGTATGGG TCTCATCATT2700
 CCCATACACA GAAACACAAA ACACTTTGAT CATAAACTTT TTTCTTCAGA AGCCAAACTA2760
 ACTTGCAGAA TAATAGAGCC ACTGGTTTAA TGTTTCCTCA AGATAGGTTT TAGTGTAAGC2820
 TAGTATTCTG TGTGTTGTA GAAATGATTC AATACCTGCA GCTGGTGAAT TAGGAATTGT2880
 ATTTGTTGCC TTTTTTATAT TAGATGAGGT GCAAAAATTT TAATGCTAGT CAGTATGCAC2940
 CACCACAGGA AAGTTAGATC CCATTAGCAC TTGAAACTAC AGCTTTGGAA ACTTAGGCTA3000
 AGTTAATTTG GATTTGTTAC TTGATTCACC TACTGACCTT TTCTTTTGT TGAAGTGCTT3060
 ATCAGCATAA TGAGCTAAGT GTCATGCATA TTTGTGAAGA AACACCCTTT TTGGTCCCTT3120
 TTGGGACAGA GAGGTACTCC TTGATCTTTA TGAATGACAG GTTACTGTTT TGCCTTATTG3180
 CTTAACCTAA TGTAGTGAAA TAAAGCAGAC AAAGCTTG 3218

(2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

GTGAGGGACA GATGGACAGA ATGCAGAGGT ACATAGATGA GCTGAGGCTG ATCCAGCTCC 60
 CCTGAAATTC AGAGTGTTAA CTTTGTAGAC CCTGCACAAT CTCTTGGTGC TATCTAGCCA120
 TTACCCCCAT TTTTTTTTTT AAGGCCATCT GAAATTCCAT TTGTCATGGT GGAAGCATT180
 TTGGATATGA TGCAGGAAAT CTCTTCCTGG AGTCAAAAGT TCCCAAGAGG TCCTGTATTT240
 TTAAGAAATG GAATTTATTT AAATAATATT TAAGCTTGTG CCCATGTTGG CCGGGCAACT300
 TTTTCAATG GTGCTTATTA GAAGAAGTTT TTTCATCTTG TCATTTTAAG AAAATAAAAC360
 TGGAAATTGA ATATGGGTGG CATGATTGTA CCCTTTTAGT TCTCTTATTT TTCTACTCCT420
 CTGTCCCTCT ATAACATATG CATACTATTA GATGCTGGTC CACTGAATGC TGAGATGATC480
 TGTTTTTTGG GGTTTTTTTT TTTTAAGAAA TATTTTCACT GGTTTTCTGT GACTCTCTAA540
 ACACTTCATC GAAACTAGGA AGACTGAATT ATGAGGGAAA CTATTTGGGA TTAGTGGCCA600
 GAAACGATGA AATCTTATAG ATCTTTTGAC AGTTTCTCTG TTTAGGGGGA GCCTAGGACT660
 GATATCCAAG TTTCTTCCAT ATCCAAGCTT CATTGGGGGA CCCCATTG GCTTTAACAG720
 GTGACCCGGC CCTCTTTACC GGGCTTCCAG 750

(2) INFORMATION ON SEQ ID NO. 393:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CACGAGGAGG CCGGGAGTGG AACCCCTCT TTTGAGAAGG TTGCCTGACT CAGAGACACA 60
 GAAACGGGTC CAGGGATGGG GAGAGATGTG GAGTGAGGGA AGGTTTGCAT TTGAGAAAGG120
 AAGTTCGAGA ACACACTGGG ACATTGTAAC ACATTGTAAC CATCTTCTGA TAGAAAGGTG180
 TTGGCCTCCT AATAATGGGA GGTCAGGGCC AGGTCCTCGG GCATAGGGAG AGGGTCCGGA240
 GAATGCTGCA GACCCCTGCC CACTGCCCCAC GGTCTCCGCT CCCTGCACCT GCCTCTGATG300
 GTGCAGCTCT GATTCCGTGT CTCTCCTCAT TGCAGATTTA TGAAGGTGCC TACCATGTTC360
 TCCACAAGGA GCTTCCTGAA GTCACCAACT CCGTCTTCCA TGAAATAAAC ATGTGGGTCT420
 CTCAAAGGAC AGCCACGGCA GGAAGTGCCT CCCCACCCTG AATGCATTGG CCGGTGCCCC480
 GCTCATGGTC TGGGGGATGC AGGCAGGGGA AGGCAGAGA TGGCTTCTCA GATATGGCTT540

GCAAAA

546

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2453 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

EST ID: 394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

CCTGACGGGA CCAAGGCGGC GGGAGTCTGC GGTGCTTCCC TCGGCTGTGG ACCGGGCGGC 60
 ACGACGCGGT GCAGGGTAAC ATGGCGGATG CGGAAGTAAT TATTTTGCCA AAGAAACATA 120
 AGAAGAAAAA GGAGCGGAAG TCATTGCCAG AAGAAGATGT AGCCGAAATA CAACACGCTG 180
 AAGAATTTTT TATCAAACCT GAATCCAAAG TTGCTAAGTT GGACACGTCT CAGTGGCCCC 240
 TTTTGCTAAA GAATTTTGAT AAGCTGAATG TAAGGACAAC AACTATACA CCTCTGTCAT 300
 GTGGTTCAAA TCCTCTGAAG AGAGAGATTG GGGACTATAT CAGGACAGGT TTCATTAATC 360
 TTGACAAGCC CTCTAACCCC TCTTCCCATG AGGTGGTAGC CTGGATTCTGA CGGATACTTC 420
 GGGTGGAGAA GACAGGGCAC AGTGGTACTC TGGATCCCAA GGTGACTGGT TGTTTAATCG 480
 TGTGCATAGA ACGAGCCACT CGCTTGGTGA AGTCACAACA GAGTGCAGGC AAAGAGTATG 540
 TGGGGATTGT CCGGCTGCAC AATGCTATTG AAGGGGGGAC CCAGCTTTCT AGGGCCCTAG 600
 AAACCTGAC AGGTGCCTTA TTCCAGCGAC CCCCACTTAT TGCTGCAGTA AAGAGGCAGC 660
 TCCGAGTGAG GACCATCTAC GAGAGCAAAA TGATTGAATA CGATCCTGAA AGAAGATTAG 720
 GAATCTTTTG GGTGAGTTGT GAGGCTGGCA CCTACATTCTG GACATTATGT GTGCACAGTG 780
 ATCAGTCACG CGCACGAGGT ACGTCAGATG CAGGAGCTTC GGAGGGTTCG TTCTGGAGTC 840
 ATGAGTGAAA AGGACCACAT GGTGACAATG CATGATGTGC TTGATGCTCA GTGGCTGTAT 900
 GATAACCACA AGGATGAGAG TTACCTGCGG CGAGTTGTTT ACCCTTTGGA AAAGCTGTTG 960
 ACATCTCATA AACGGCTGGT TATGAAAGAC AGTGCAGTAA ATGCCATCTG CTATGGGGCC1020
 AAGATTATGC TTCCAGGTGT TCTTCGATAT GAGGACGGCA TTGAGGTCAA TCAGGAGATT1080
 GTGGTTATCA CCACCAAAGG AGAAGCAATC TGCATGGCTA TTGCATTAAT GACCACAGCG1140
 GTCATCTCTA CCTGCGACCA TGGTATAGTA GCCAAGATCA AGAGAGTGAT CATGGAGAGA1200
 GACACTTACC CTCGGAAGTG GGGTTTAGGT CCAAAGGCAA GTCAGAAGAA GCTGATGATC1260
 AAGCAGGGCC TTCTGGACAA GCATGGGAAG CCCACAGACA GCACACCTGC CACCTGGAAG1320
 CAGGAGTATG TTGACTACAG TGAGTCTGCC AAAAAAGAGG TGGTTGCTGA AGTGGTAAAA1380
 GCCCCGACAG TAGTTGCCGA AGCAGCAAAA ACTGCGAAGG GAAGCGAGGA GAGTGAGAGT1440
 GAAAGTGACG AGACTCCTCC AGCAGCTCCT CAGTTGATCA AGAAGGAAAA GAAGAAGAGT1500
 AAGAAGGACA AGAAGGCCAA AGCTGGTCTG GAGAGCGGGG CCGAGCCTGG AGATGGGGAC1560
 AGTGATACCA CCAAGAAGAA GAAGAAGAAG AAGAAAGCAA AAGAGGTAGA ATTGTTTTCT1620
 GAGTAGTGAA GGCCACTTGA AGCTGGAGGA GAAACTAAAG CCTTATTGAG AAAACATGTT1680
 ATAGATCCTT TTGTTGCTGA GAGAGTGGAA CATAGGTCCT AGACAGGGTG AAGAGTTCTG1740
 GCACATTTTA GCTGCTACTT TGAGACCTCG GTGATGTTAC CTGGTGTGGT CATCCCATCT1800
 TGTCTGTTT TAAGGATATG GGTGGTGAAA GATGAAAGAG GCAGAGTTTA TCCCAATGAC1860
 TTCTCTGTTT GAGTTGGGAA GCCTCACCTT CAGACCCAGT AACTGTCCGC AGCTGTCTGC1920
 TAGTGGTTGT CTTAACATCG TAGTCCTAGT TTGCATTTTT TAAATCCCCCT CTGTTTAAAA1980
 GGTTTGTAAA AAAAAACAA AAAACTAAGT CTGCTCAGTG AAATGCTGTA GAACCCTAAA2040
 TAAGTGGTAG AAGAGTGTC CTGAATTTTG TCTCTGAATT CAGTATAACT GAGTTTGTGC2100
 CATGCTGGTG TCTGGGTTAT AGGCCTGATG GGCCTGGTAG TTTTCCATCT TGTTCTGGCC2160
 TAGAGGTCAG TCCTTTGCAC TTCCTCAAAG CTTGTGTACA GTGCTCACCT AAATCCATCT2220
 GACTACTTGT TCCTGTGCCC TCTTGTTTTA GGCCTCGTTT ACTTTTAAAA AATGAAATTG2280
 TTCATTGCTG GGAGAAGAAT GTTGTAAATTT TTAATTATTA AAGTCAACTT GTTAAGTTTT2340
 TTATGTATTC CTGTTGGGTT TTCTTGTGTA TCTCATGCTA GCAGAGCAAA AATTGTAAAA2400
 TATTTTGATT AAAAATCTAG GGACCTTTAT GTCCTATTTG AAAAAA AAA 2453

1999-09-24 14:55:00

(2) INFORMATION ON SEQ ID NO. 395:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2706 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

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GGGAGGAAGG AGACTACACC TGCTTTGCTG AAAATCAGGT CGGGAAGGAC GAGATGAGAG 60
TCAGAGTCAA GGTGGTGACA GCGCCCGCCA CCATCCGGAA CAAGACTTAC TTGGCGGTTT 120
AGGTGCCCTA TGGAGACGTG GTCACGTAG CCTGTGAGGC CAAAGGAGAA CCCATGCCCC 180
AGGTGACTTG GTTGTCCCCA ACCAACAAGG TGATCCCCAC CTCCTCTGAG AAGTATCAGA 240
TATACCAAGA TGGCACTCTC CTTATTGAGA AAGCCCAGCG TTCTGACAGC GGCAACTACA 300
CCTGCTTGGT CAGGAACAGC GCGGGAGAGG ATAGGAAGAC GGTGTGGATT CACGTCAACG 360
TCCAGCCACC CAAGATCAAC GGTAACCCCA ACCCATCAC CACCGTGCGG GAGATAGCAG 420
CCGGGGGCGAG TCGGAAACTG ATTGAGTGCA AAGCTGAAGG CATCCCCACC CCGAGGGTGT 480
TATGGGCTTT TCCCGAGGGT GTGGTTCTGC CAGCTCCATA CTATGGAAAC CGGATCACTG 540
TCCATGGCAA CGGTTCCCTG GACATCAGGA GTTTGAGGAA GAGCGACTCC GTCCAGCTGG 600
TATGCATGGC ACGCAACGAG GGAGGGGAGG CCAGGTTGAT CCTGCAGCTC ACTGTCCTGG 660
AGCCCATGGA GAAACCCATC TTCCACGACC CGATCAGCGA GAAGATCACG GCCATGGCGG 720
GGCCACAACA TTCAGCCTCA ACTGCTCTGC CGCGGGGACC CCGACACCCA GCCTGGTGTG 780
GGTCCTTCCC AATGGCACCG ATCTGCAGAG TGGACAGCAG CTGCAGCGCT TCTACCACAA 840
GGCTGACGGC ATGCTACACA TTAGCGGTCT CTCCTCGGTG GACGCTGGGG CCTACCGCTG 900
CGTGGCCCGC AATGCCGCTG GCCACACGGA GAGGCTGGTC TCCCTGAAGG TGGGACTGAA 960
GCCAGAAGCA AACAAGCAGT ATCATAACCT GGTCAGCATC ATCAATGGTG AGACCCTGAA1020
GCTCCCCTGC ACCCCTCCCG GGGCTGGGCA GGGACGTTTC TCCTGGACGC TCCCCAATGG1080
CATGCATCTG GAGGGCCCCC AAACCCTGGG ACGCGTTTCT CTTCTGGACA ATGGCACCCT1140
CACGGTTCGT GAGGCCTCGG TGTTTGACAG GGGTACCTAT GTATGCAGGA TGGAGACGGA1200
GTACGGCCCT TCGGTCACCA GCATCCCCGT GATTGTGATC GCCTATCCTC CCCGGATCAC1260
CAGCGAGCCC ACCCGGTCA TCTACACCG GCCCGGGAAC ACCGTGAAAC TGAAGTGCAT1320
GGCTATGGGG ATTCCCAAAG CTGACATCAC GTGGGAGTTA CCGGATAAGT CGCATCTGAA1380
GGCAGGGGTT CAGGCTCGTC TGTATGGAA CAGATTTCTT CACCCCCAGG GATCACTGAC1440

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CATCCAGCAT GCCACACAGA GAGATGCCGG CTTCTACAAG TGCATGGCAA AAAACATTCT1500
 CGGCAGTGAC TCCAAAACAA CTTACATCCA CGTCTTCTGA AATGTGGATT CCAGAATGAT1560
 TGCTTAGGAA CTGACAACAA AGCGGGGTTT TTAAGGGAAG CCAGGTTGGG GAATAGGAGC1620
 TCTTAAATAA TGTGTCACAG TGCATGGTGG CCTCTGGTGG GTTTCAGTT GAGGTTGATC1680
 TTGATCTACA ATTGTTGGGA AAAGGAAGCA ATGCAGACAC GAGAAGGAGG GCTCAGCCTT1740
 GCTGAGACAC TTTCTTTTGT GTTTACATCA TGCCAGGGGC TTCATTTCAGG GTGTCTGTGC1800
 TCTGACTGCA ATTTTCTTT TTTTGCAAAT GCCACTCGAC TGCCTTCATA AGCGTCCATA1860
 GGATATCTGA GGAACATTCA TCAAAAATAA GCCATAGACA TGAACAACAC CTCCTACCC1920
 CATTGAAGAC GCATCACCTA GTTAACCTGC TGCAGTTTTT ACATGATAGA CTTTGTTCCT1980
 GATTGACAAG TCATCTTTCA GTTATTCCTC TGTCACCTCA AAACCTCCAGC TTGCCAATAA2040
 GGATTTAGAA CCAGAGTGAC TGATATATAT ATATATTTTA ATTCAGAGTT ACATACATAC2100
 AGCTACCATT TTATATGAAA AAAGAAAAAC ATTTCTTCCT GGAACCTCACT TTTTATATAA2160
 TGTTTATAT ATATTTTTT TCCTTTCAA GCAGCATG AGACTAGAAG GAGAAATACT2220
 TTCTGTCTTA TTAAAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280
 GACATGGAAA TATAATTTTA AAAAATTTCT CTCCAACCTC CTTCAAATTC AGTCACCACT2340
 GTTATATTAC CTTCTCCAGG AACCTCCAG TGGGGAAGGC TGCGATATTA GATTTCTTG2400
 TATGCAAAGT TTTTGTGAA AGCTGTGCTC AGAGGAGGTG AGAGGAGAGG AAGGAGAAAA2460
 CTGCATCATA ACTTTACAGA ATTGAATCTA GAGTCTTCCC CGAAAAGCCC AGAACTTCT2520
 CTGCAGTATC TGGCTTGTCC ATCTGGTCTA AGGTGGCTGC TTCTTCCCCA GCCATGAGTC2580
 AGTTTGTGCC CATGAATAAT ACACGACCTG TTATTTCCAT GACTGCTTTA CTGTATTTTT2640
 AAGGTCAATA TACTGTACAT TTGATAATAA AATAATATTC TCCCAAAAAA AAAAAAAAAA2700
 AAAAAAG 2706

(2) INFORMATION ON SEQ ID NO. 396:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2242 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

CAGGCCGGTT CCGGCGAAGT TAAACCCTCG GAGCTGGCCT CGGACTGCTG GGGCGTTACC 60
 CCTTCGGCCA CCCCCGCTGA CCATGGCAGT GTTTCATGAC GAGGTGGAAA TCGAGGACTT 120
 CCAATATGAC GAGGACTCGG AGACGTATTT CTATCCCTGC CCATGTGGAG ATAACCTCTC 180
 CATCACCAAG GAAGATTGGG AGAATGGGGA AGACGTGGCA ACGTGTCCCTA GCTGCTCTCT 240
 CATTATAAAA GTGATTATTG ACAAAGATCA GTTTGTGTGT GGAGAAACAG TCCCAGCCCC 300
 TTCAGCCAAC AAAGAATTAG TTAAATGCTG AAGAAGCCTT CAGGAATCCA AATCCTGAAC 360
 ATTTGGAATG AGCCCAGATA GAAATATCGA ATGCAAAGCT ACTGGCTTCA CAGAGACAAC 420
 CATTTATGAT TTGCTGTTCT GTAAGAGTGT GGATTCTTTC TATCAACTGC TGATATCATC 480
 TTCAGGAAGC AAGTCCATAA CATGACATAT CTGGATTTTG TGCTTAGAAC CTTAAATTGG 540
 AAGCATTCTT AATTATGCAT CTAAATTTAA AAGAAGATAA TTTCAAAACA GTGCTTTCTT 600

 TCCCTTGGTT TCATCATTTT CATATCTTAA ACCAAATTAC TTCGGTATCT GACAACAGCA 660
 TCATCTACCT CAGTCATTAG GATTTCTTAA TAAAAAAGAG ATTGTATTTT TGACTTGGTT 720
 ATTAAGATTA TTAAATTAG CCTTCCCTTT GAAATATGAC ATCAGCTTTG CTGTTCTAAA 780
 TTTAAATTA GTTGCTTCAT CAGTACCACA CTTCCAGTTT CTATACCAAG CCAGTCTCCT 840
 CAGTTTTCCC ATTAGAATGG ACATGTTCTG TTCAGCGTGT CATTCTGTGA ATGCTTCATG 900
 CAGAGAGTTT GGTTCATAGTA TTAAAGAGAA AATACAGTGA GGTCACAATG TCTCCAGAGC 960
 TAAAGATTAG TGAACAAGAA AGAAAGTCCA AAATGAAGTG ATGAAAGAAT GAGGACTTTTT1020
 CTTATATTCT GCATATTCCT TGGAAGTCAG GACAAGATGA AAAGAAAAAC ATCCAAAAGA1080
 AGTGAAATTG GTGACAGAAT GAGAGGAGCA AAGCATACCA GTGTAGTAAG TGGAAATGTTT1140
 GAATGACTTT GCCAGGTCAG AGCAAGTAAT ATTTCTGTAT CTGAGTTTTT GTTTGTGTTT1200
 TGATAAGGCT AATGAAATTG CATTCCAGGT AGGGGTAAAC GTCAAATTTT CATGGCTGGT1260
 AGCTGTGCTT TTGGCATATC ACAGTGTTGT GTCACTACTA CAAGGTAAAG CATCTACAGC1320
 GGAGAATGAG CTTGAAAATG AGAGACCTAT TGTGAATAAA TATGCCCATG AGAGCATATT1380
 TAATAAGCCT CTATAACATG CAGCCAAACC AGACATTCAC TCCTGCAGAG AAATGTTGCC1440
 CTGGAGAAAA AGAGATATAT AAAGATAGGC TATCACCCCTT CTTTGTGCTGC AGTACTAAGC1500
 ATAGCAAGAA ATTAGAATCA TTTACATTGG AAATTGAAA ATTCCCTTTA TATACACAAC1560
 TTTACTGTGT ATAAATAAAA AATATTTATT AATGCAGTGA TGTCCGTCAG GTTGTTTTAG1620
 GAATGGCTTC TGCAATTAGA AAAATAGCTT GCTAGAATGT AAATGTTCTG CTACTGGTAA1680
 ATGTACTGCA CACATTCATT GGACGTAAAA ACAAGTGAGT AGCCTTTTTT ACCTGCCAGC1740
 AGCATGGCTG TGTGCAGCCA CTAGGCTGAG ACAATAAATT ACCAAAAATT ATAATGTACC1800
 GAGCTGAAAA TGCTCAGTAC ATTATGTGGC ATATTCTGGA TGTGATGAGA AATCTCATTG1860
 CCATTTGGGA CACTGACATC CCAGAAGTAA TCCACAACCTG CTTTGCAAAA GCAAAGTGAC1920
 TGCTCAGATG AACAGAGCAG AGTACTCACT CACTATGGTG GCATCAGCTG CAAAGCGAAA1980
 TGAAGTGTCC CATGATCATG TTGATGGTTT TCTAGATACT GCCAACATGT TAGCTCTTTC2040
 TGATGCTGAT GAGTTTCAA CACGAACAGA CACCTTGAT GTGGGTTTGC TAAGAACATA2100
 GAAGAACAGG AAGAAAAGTT GCCAGGGTTT AAAAATCCCA GGGAAAAAAG AAGCATAAAA2160
 AGCATTAGCA GTCAGTGACT GATGATAATG CTTGCAATAA TGGGGAATGG TTTTGTTC2220
 TAAAACCCAA AATTTATTTT TT

2242

"00000" 04952950

(2) INFORMATION ON SEQ ID NO. 397:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

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TAGTCATCCT ACAAACATGT TTCTGTTACT TCCTAATATT AAAATAGCCA TTTTGGATTG 60
CATATTTAAA GTGCTCATTT GAGTGAAATT CAAATTAGAA AGAAAGATAT TAAAATGCGC 120
CTAACAAAAA CCTCTCTTTC AGAATCCCTA TTCCTTGAAT CTTGGGTTTG AACTGCTTAT 180
TAAAGGCAGG CCTAAACTAA TTTGTGAGAA ATGAAGAAGT TTTAGTATAT AATTCCTTTA 240
AAAAATATCA ATTACGGCTG GGTGCGGTGG CTCAGGCCTG TAATGCCAGC ACTTTGGGAG 300

GCCAAGGCGG GTGATCACCT GAGGTCAGGA GTTCAAGACC AGCCTGGCCA ACATGGCAAA 360
ACCCTGTCTC TACTAAAAAG TAAAAAAAT TAGCCGGGCA TGGTGGCTTG TGCTTGTAGT 420
CCCACTTCAG TCTAAGTAGC TGGGACTACA GGCACGTGCC ACNAGGCCCA GCTAATGTGG 480
GTGTTTTGTT AGAGATGAGG TAGGGCCATA TTGCCAGGC TCGTCTTGAA CACCGGGGCT 540
CAAGGAATCT GCCCATCTTC GCCTCCCAA GTTCTGAGAT AGCAGGTGTG AGTCANTCAT 600
GCCCAGCCTC CTTGAAGTTT ACTAACAATT GGGATAACTG AGGGAAGAGA AGTGACAATT 660
CCACTCAGTC TATTAGAGGT CTGGATATAA GGTAGNCCAC ACAATAACTC TAACNTTGAC 720
TTCTAACCAT TCTATCTTAT TGNATTGGA GGCTGTCTTC TGNCCAGATT TTTTGTGGCT 780
TGAGATGATA TTTTNCGAAC CCTTCTTCA CTACCTTTCT TACCCTTAAT GTGNCCAAGC 840
TTGAAACAGG ATTTGATTTT CTGAGCNTAC TTGTTGNGCC TTCTGTGCGT CANCCAAGTA 900
ATCTGGTTCA TCTTNCGTN CTCATTCATG TTATTTTCAA GTGAAACAAG ACATTTTGGG 960
GGNTCAAGTC TCNTTTGGGN NTGTTTGTG TTTATGTATA TAAAAATGGA TTTTGNTGTT1020
CCCTTTCCNA TGTNAAGTAN CCAACTTATA TGGAACTCA CAATCATAAT GTAAAGAAGA1080
AATGAAANGC CTGGTGTATT GTACTTCAAG ATGCCTCCCT GNATGTATAG AATCNTCCTT1140
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TTAGAATTTT TAAATACCAA CTATAAAAAA AAAAAAAA 1239

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"9999" 9999 9999

(2) INFORMATION ON SEQ ID NO. 398:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

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GAACCTGCTC TCCTGCTTGC TGGTCCCTTG ACGCAGAGAC CGTTGCCTCC CCCACAGCCG 60
TTTGACTGAA GGCTGCTCTG GAGACCTAGA GTAAACGGC TGATGGAAGT TGTGGGACCC 120
ACTTCCATTT CCTTCAGTCA TTAGAGGTGG AAGGGAGGGG TCTCCAAGTT TGGAGATTGA 180
GCAGATGAGG CTTGGGATGC CCCCTGCTTT GACTTCAGCC ATGGATGAGG AGTGGGATGG 240
CAGCAAGGTG GCTCCTGTGG CAGTGGAGTT GTTGCCAGAA ACAGTGGCCA GTTGTATCGC 300
CTATAAGACA GGGTAAGGTC TGAAGAGCTG AGCCTGTAAT TCTGCTGTAA TAATGATAGT 360
GCTCAAGAAG TGCCTTGAGT TGGTGTACAG TGCCATGGCC AGCAAGAATC CCAGATTTCA 420
GGTTTTATTA CAAAATGTAA GTGGTCACTT GGCGATTTTG TAGTACATGC ATGAGTTACC 480
TTTTTCTCT ATGTCTGAGA ACTGTCAGAT TAAAACAAGA TGGCAAAGAG ATCGTTAGAG 540
TGCACAACAA AATCACTATC CCATTAGACA CATCATCAA AGCTTATTTT TATTCTTGCA 600
CTGGAAGAAAT CGTAAGTCAA CTGTTTCTTG ACCATGGCAG TGTTCCTGGCT CCAAATGTGA 660
GTGATTCCAA ATAATGGTTC TGTTAACACT TTGGCAGAAA ATGCCAGCTC AGATATTTTG 720
AGATACTAAG GATTATCTTT GGACATGTAC TGCAGCTTCT TGTCTCTGTT TTGGATTACT 780
GGAATACCCA TGGGCCCTCT CAAGAGTGCT GGACTTCTAG GACATTAAGA TGATTGTCAG 840
TACATTAAAC TTTTCAATCC CATTATGCAA TCTTGTTTGT AAATGTAAAC TTCTAAAAAT 900
ATGGTTAATA ACATTCAACC TGTTTATTAC AACTTAAAAG GAACTTCAGT GAATTTGTTT 960

TTATTTTTTA ACAAGATTTG TGAAGTGAAT ATCATGAACC ATGTTTTGAT ACCCCTTTTTT1020
CACGTTGTGC CAACGGAATA GGGTGTTTGA TATTTCTTCA TATGTTAAGG AGATGCTTCA1080
AAATGTCAAT TGCTTTAAAC TTAAATTACC TCTCAAGAGA CCAAGGTACA TTTACCTCAT1140
TGTGTATATA ATGTTTAATA TTTGTCAGAG CATTCTCCAG GTTTGCAGTT TTATTTCTAT1200
AAAGTATGGG TATTATGTTG CTCAGTTACT CAAATGGTAC TGTATTGTTT ATATTTGTAC1260
CCCAAATAAC ATCGTCTGTA CTTTCTGTTT TCTGTATTGT ATTTGTGCAG GATTCTTTAG1320
GCTTTATCAG TGTAATCTCT GCCTTTTAAG ATATGTACAG AAAATGTCCA TATAAATTTT1380
CATTGAAGTC GAATGATACT GAGAAGCCTG TAAAGAGGAG AAAAAACAT AAGCTGTGTT1440
TCCCCATAAG TTTTTTTAAA TTGTATATTG TATTTGTAGT AATATTCCAA AAGAATGTAA1500
ATAGGAAATA GAAGAGTGAT GCTTATGTTA AGTCCTAACA CTACAGTAGA AGAATGGAAG1560
CAGTGCAAT AAATTACATT TTTCCAAAA AAAAAAAAAA AAAAAAGTGT1620
ATACGTTGGA ATGAAAAAAA AAAAAAAAAA AAAAAAAA AAA 1663

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(2) INFORMATION ON SEQ ID NO. 399:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2889 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

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GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60
GAAAAACTTC CAGATGGCTT CTATCACATC CCCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120
AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTCTCTGT 180
TCTCTTCATG AAAGTGTTCT TGCCCAAGGA GGAATTGTAC ATGCCCCCAC TGGTGATCAA 240
GGTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTCGTC GGCCAGTGCA CCATCGAGCG 300
CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAAGAG GACATCGTCC CACAGCTCAA 360
AGCCTCCCTG CTGTCTGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA 420
ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGAAT GGTGGAGTAA 480
ATTTGATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTCAGA AAGGCTATTC 540
CAAGCTCAAG ATATATAATT GTGAAGTAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600
CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660
GGTTGGAGAG TTTAAGGGCT CCTTTCGGAT CTACCCTCTG CCGGATGACC CCAGCGTGCC 720
AGCCCCCTCC AGACAGTTTC GGGGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780
GATTTACATT GTTCGAGGCT TAGAGCTCCA GCCCCAGGAC AACAAATGGCC TGTGTGACCC 840
TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900
CACTCTCAAC CCAGTCTTTG GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAAGAAAA 960
AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA1020
AACAATTATT GATCTGGAAA ACCGATTCTT TTCCCGCTTT GGGTCCCACT GCGGCATACC1080
AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT1140
GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG1200

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TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAATCCT1260
 GCACCAGCAC CTCGGGGGCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG1320
 GCTGGTCCCT GAGCACGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTT1380
 CCAGGGAAAA CTTCAGATGT GGGTGGATGT TTTCCCAAG AGTTTGGGGC CACCAGGCC1440
 TCCTTTCAAC ATCACACCCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA1500
 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560
 CGTCAAAGGC TGGATTCTTG GCAATGAAGA AAACAAACAG AAAACAGATG TCCATTACAG1620
 ATCTTTGGAT GGTGAAGGGA ATTTTAACTG GCGATTTGTT TTTCCGTTT ACTACCTTCC1680
 AGCCGAACAA CTCTGTATCG TTGCGAAAA AGAGCATTTC TGGAGTATTG ACCAAACGGA1740
 ATTTCGAATC CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA1800
 TGACTIONTG GGTTCCTAG AACTTGACTT GCGTCACACG ATCATTCTTG CAAAATCACC1860
 AGAGAAATGC AGGTTGGACA TGATTCCGGA CCTCAAAGCC ATGAACCCCC TTAAAGCCAA1920
 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA1980
 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAAATCC TCAACGAGAA2040
 GGAGGCCGAC GAGAGGCCAG CCGGGAAGGG GCGGGACGAA CCCAACATGA ACCCCAAGCT2100
 GGACTTACCA AATCGACCAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT2160
 GAAGTTCATC GTGTGGCGCC GCTTTAAGTG GGTCAATCAT GGCTTGCTGT TCCTGCTTAT2220
 CCTGCTGCTC TTCGTGGCCG TGCTCCTCTA CTCTTTGCCG AACTATTTGT CAATGAAGAT2280
 TGTAAAGCCA AATGTGTAAC AAAGGCAAAG GCTTCATTTC AAGAGTCATC CAGCAATGAG2340
 AGAATCCTGC CTCTGTAGAC CAACATCCAG TGTGATTTTG TGTCTGAGAC CACACCCAG2400
 TAGCAGGTTA CGCCATGTCA CCGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCCTGGAAA2460
 GTCAGGCCAA CAAGCAACGT TTGCATCATG TTATCTCTTA AGTATTAAAA GTTTTATTTT2520
 CTAAAGTTTA AATCATGTTT TTCAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580
 CATCTTTTTA TATGTGTCTT CGGTTCTAGA CTTCAGCTTT TGGAAATTGC TAAATAGAAT2640
 TCAAAAATCT CTGCATCCTG AGGTGATATA CTTCATATTT GTAATCAACT GAAAGAGCTG2700
 TGCATTATAA AATCAGTTAG AATAGTTAGA ACAATTCTTA TTTATGCCCC CAACCATTGC2760
 TATATTTTGT ATGGATGTCA TAAAGTCTA TTAACTCT GTAAATGAAAC TAAATAAAAA2820
 TGTTTCACCT TTAACATA GGGGGGGTGG TCGGGGGGTC GGGAGGGGG GGGGTGGTGT2880
 GGGGTGTGG 2889

(2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1774 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

TGAAGGAAGT AACAAAAGTG GGAAACCCCT GATAAACCCC CTCAGGATCC TCATGGAGAA 60
 CTTACCTATC CAGGAGAAAT AGCAAAGGGG AAAGAACTGG CCCCCCCTG ATTCCGATGA 120
 CCCTCCCCC GGGTCCCCCTC CCCACAACAT GTGGGAATTC CCAGAAGATA AATTCAAGTT 180

 GCAATTTTCAG TGGGGACATA GCCCAAACCC ATATCACTGG TGATGCCAC TTCTTCAGTA 240
 TTAGGGATTTC TCAGTCAGAA GAGACCCCT GTGTGGCCTG AGTCCCTCA GGAGGAAGGT 300
 GGACAACAGA GAAATGAGAG TTTTGATATT TTCTGAAAGA GGAACATGTG TTAGAGATGA 360
 AGAATCTTCC AAGGCTCATG CAGTTGCTTA GAATAATCAT TACTGTTATA TGAGAAACAT 420
 TTTAGTAATT TAATAAAAGG ATAATGTTTA TTTAAAAAAC CTGACTTTC CAGAGTAATT 480
 TTGTTTTGCA CATTTCATGTT TATTGAAGTG GACTAATTC TATAATGCAA ATCAGAGTTA 540
 AATATTAAAA ATTGTGTAAA TACAATTGAC ATAGGAATTA CATTAAAAATA TTAGGAAGAA 600
 ACAAGGACAA ATTTAGACCT TGAATCCGAA GAGATAAAGC TTACTTGACT TTCAAATGGA 660
 GAGATGATGA AAACCCACTC ATTCAGTCTT TCAGAACAAA AAGACAGTCA TCTGATAAGA 720
 GTATGACATG GATGAAATGC CCTACAGGGG CCTTGGACAT CTTAATTTTC TGCGATTATG 780
 TGAAAGAGGT GGACTTTACA GATAATGGAG CAGAAGCCAA CATTAGTAAA AGGAATCCCA 840
 ACTTCTTCCC ATAGAATTAG AAACATGTGA AAGTACAATA AACTTCTTGT TCAAATTACC 900
 AGCATCAGAG AGCTTCCCAT TTGCATCTAG ACCTTGAATT TATATTTATT GATCAAGTTC 960
 TAATTTGTAT GTATATTTTG TGCATATTCA CCAATAACAG TTAAAATTAA TTATGTGTTA1020
 TAGTTAATAT ATGCACCTAC CTTCTTCCGT TAGTGCATCA GTAAATGTGT TATTTGTCA1080
 TTTTTCAAA GAGAGTGTTG TAGGTTTTCC CTGTAGTTCT TCCTTTATAG CTTTCTTCT1140
 GATAACCATG ACTTCAGGAG CTTTAAACT ATCTATCTTG CATTGTGTC TGGCGGAGAA1200
 CTAGCCATCA GCCTCCTGAA GCCTGCCATC ATTGTTAATT TGAGGACTGG GCTGTCTTGG1260
 GGCTCAGAAG GTAAAGAACT ATTTGAGCAG ATGTGTGTGG GTGGCACTGG ATTCCACCCA1320
 ACTGCCAAGT TAGTATTGTT AGAGATTTCA TTTTACAACA CAAAAATAAG CCTGTGTCAA1380
 AGATTTTAAA ATCATGGAAA GTTAAATCT AGAAAGACCT TAGAGAACCA GCCAACCAAC1440
 TCTCTCATTT TAAAAGTGAA GGATTCATAG CACAGATTAC TTGCCTAAGA TCATCCAGGA1500
 ACGAAGACAA GAATCCAAAT GTACTTGGGG ACAAGAATTA GTCCCCAAAT TCAGTGTTCT1560
 TCCTAGTATT AAACATTGCC CTTTTCGACA AATTTTGGAT TTCAATCTTG GTATATTTCA1620
 GTAAACCTGC TGATTTATTA GGTTACTGGG TAGATGACAT TAGAATGTAG ATAGCGTGCA1680
 CGCTATGATA GACTCTGCTA AGACATGTTT CCAGTGTTCA GCAGCAATGT AGATATGTGT1740
 GACAGTGGTC ATGTAGAAGT TATAAAGCAG AGTA 1774

(2) INFORMATION ON SEQ ID NO. 401:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3982 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

CCCAAGTGTG ATGCATTGTT CTTCAGATGT TGAAAAGAAA GCAAAAAATA CCTTCTAACT 60
 TAAGACAGAA TTTTAAACAA AATGAGCAGT AAAAGTCACA TGAACCACTC CAAAATCAGT 120
 GCATTTTGCA TATTTTAA CAAAGACAGC TTGTTGAATA CTGAGAAGAG GAGTGCAAGG 180
 AGAAGGTCTG TACTAACAAA GCCAAATTCC TCAAGCTCTT ACTGGACTCA GTTCAGAGTG 240
 GTGGGCCATT AACCCCAACA TGGAATTTTT CCATATAAAT CTCAATGAAT TCCCTTTCAT 300

 TTGAATAGGC AAACCCAAAT CCATGCAAGT GTTTTAAAGC ACTGTCCTGT CTTAATCTTA 360
 CATGCTGAAA GTCTTCATGG TGATATGCAC TATATTCAGT ATACGTATGT TTTCTACTT 420
 CTCTTGTAAG ACTGTTGCAT GATCCAACCT CAGCAATGAA TTGTGCCTAG TGGAGAACCT 480
 CTATAGATCT TAAAAAATGA ATTATTCTTT AGCAGTGTAT TACTCACATG GGTGCAATCT 540
 TTAGCCCCAG GGAGGTCAAT AATGTCTTTT AAAGCCAGAA GTCACATTTT ACCAATATGC 600
 ATTTATCATA ATTGGTGCTT AGGCTGTATA TTCAAGCCTG TTGTCTTAAC ATTTTGATA 660
 AAAAAGAACA ACAGAAATTA TCTGTCATTT GAGAAGTGGC TTGACAATCA TTTGAGCTTT 720
 GAAGCAGTCA CTGTGGTGTA ATATGAATGC TGTCCTAGTG GTCATAGTAC CAAGGGCAGC 780
 TGTCTCCCCT TGGTATAACT GATTTCCCTT TTAGTCCTCT ACTGCTAAAT AAGTTAATTT 840
 TGCATTTTGC AGAAAGAAAC ATTGATTGCT AAATCTTTT GCTGCTGTGT TTTGGTGTGT 900
 TCATGTTTAC TTGTTTTATA TTGACTGTTT TAAGTATGAG AGGCTTATAG TGCCCTCCAT 960
 TGTAATCCA TAGTCATCTT TTTAAGCTTA TTGTGTTTAA GAAAGTAGCT ATGTGTTAAA1020
 CAGAGGTGAT GGCAGCCCTT CCCTAGCACA CTGGTGGAAG AGACCCCTTA AGAACCTGAC1080
 CCCAGTGAAT GAAGGTGATG CACAGGGAGC ACCAAAGGAC CTTCGTAAAG TGATAATTGT1140
 CCTGGCCTCT CAGCCATGAC CGTTATGAGG AAATATCCCC CATTGGAAT TAACAGATGC1200
 CTCCTCTCCA AAGAGAATTA AAATCGTAGC TTGTACAGAT CAAGAGAATA TACTGGGCAG1260
 AATGAAGTAT GTTTGTTTAT TTTTCTTTAA AAATAAAGGA TTTTGGAAT CTGGAGAGTA1320
 AGATATAGTA TAGAGTTTGC CTCAACACAT GTGAGGGCCA AATAACCTGC TAGCTAGGCA1380
 GTAATAAACT CTGTTACAGA AGAGAAAAAG GGCCGGGCAC AGTGGCTTAT TCCTGTAATC1440
 CCAACACTGT GGAAGGCCGA GGCAGGAGGA TCACTTGAGT CCAGGAGTTT GAAACCTACC1500
 TAGGCAACAT GGTGAAACCT TGTCTCTACC AAAATAAAAA TTAGCTGGGC ATGGTGGCAC1560
 GTGCCGTGGG TCCCAGCTAC TTGGGAGGCT GAGGTGGGAG CCTGGGAGGT CAAGGCTGCA1620
 GTGAGCCATG ATCATGCCAC TGCACTCCAT CCTGGGTGAC AGCAAGATCT TGTAATAAAA1680
 AAAAAAAAAA AAACCAGGAG TGAAAAAGGA AAGTAGAAGG CAGCTGCTGG CCTAGATGTT1740
 GGTGTTGGGAA TATTAGGTGA TCCTGTTGAG ATTCTGGATC CAGAGCAATT TCTTTAGCTT1800
 TTGACTTTGC CAAAGTGTAG ATAGCCTTTA TCCAGCAGTA TTTTAAGTGG GGAATGCAAC1860
 GTGAGGCCAA CTGAACAATT CCCCCGTGG CTGCCAGAT AGTCACAGTC AAGGTTGGAG1920
 AGTCTCCTC CAGCCAGTGA CCTACCCAAA CCTTTTGTTT TGTAATAACTG CTCTGGAAAT1980
 ACCGGGAAGC CCAGTTTTCT CACGTGGTTT CTAGCTTCTT CAGACTCAGC CCAAATTAGG2040
 AAGTGCAGAA GCACATGATG GTGAAAAACC TAGGATTTGG CAGCCTTCCA GAATGGTATG2100

"09922950" 09922950

GAATCTGAGG GAAGATTTAT GTTTCGTTTT GGAGGATAGC TCAAGTTGAA TTTTCTTTCC2160
 AGCCAGTTAC CCTTTCAACC TACCCATACT TTGTACAAC CTTACACAAA TACTTAGATA2220
 TTTATTAGAT AGCCCTGAAT TCACTCTAAT TATAAACAGG GAGTGTAAC TGCCCCCAGA2280
 TGTTCTTGGG CTGGGTAAAA GCAGCTGGAG TGAAGCACTC ATTTTCCATA AAGGTAACAA2340
 AGGGCAGCTC AGTGGTTACT CAAGCTCAAA AGGGTTTTTT TAAGAGCAAG CATTGGTTAA2400
 GTCTGTGTAT ACTGAGTTGG AAGTGATTTC AGCACATTCT TTTTLAGTGG AGTGAAAGTT2460
 CTGAAGCCCC CTTTAACTT CCTCTTGGTT TTTTATTATA ATTGGTAGCC ATCTCATGAA2520
 CTGTCTCTGA CTGTTGTCTC TTTGTGGTCA TGTGATTGTG AGCTTGCTTT CTGACTTGCA2580
 TTTCTGACTT TATCCTGTTG TTAGGAAGAT AGAACTAGG TTTTGAAAGA TTACATGATT2640
 CAAGCGAGGG ATTTTAAAGT AAAGATGTAT TTATTCTGAA GAATCTAAAA GATAACAGAT2700
 TATTTGCTTA TGAAAGAACA ATATAGTCTG GGAATCCAG AATGTCAAGC CAAAGGTCTA2760
 AGAAGTCATC TCCTTCAAA ACTTTAATAA AGAAGTATTT CGAGGAGATA TCTGTCCAAA2820
 AAGGTTTGAC TGGCCTCCAG ATTCCAGTTA TTTTAAAAA GCAACTTACC ACTAAATCCT2880
 TGAGTCTCCA TAGAGTAACA GTAAAGAAAC TGTAGTAACA GACTCTCCTC TCAAAGGATC2940
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 GAGCTTGCAT CCTGGAGACT AAAGATTGCA CTTTTTTGTA GTTTTTTGTC CAAATGCAAT3060
 CCCATTTCTG TGCCTCTTAG CATGCAGTTA GATTTGGACA AACAAGATTC CTAAGGAATG3120
 ACTTTATTAA CTATAATATG GTTACAGCTA TTATATAAAT ATATATTCTG GTTATAGTTC3180
 TAATATGGAG ATGTTGTGTG CAATGCTGGC CTGTGGTGGT CTGTGTAATG CTTTAACTTG3240
 TATGGAGGAG GCCAGGCTCA GAGCTGAGAT GTGGCCTGAA CCTTCCCTGT ATCGATCCTT3300
 TAATTTAGAA CTGTCAAGAT GTCACCTTCT CCCCCTCTGC CTTTTAGTGG TATCTGACAT3360
 ATACTCAAAA CAGTAATTTT CTGGTCACAT CATTAACTGC TAATTCTGTA TTTATAAAGA3420
 ATTTTCAGAT GGACATGTAC AAATTTGAAC TCAAACCATC CCCAGTCCAG ATACAGGGCA3480
 GCGTGTAGGT GACCACACCA GAGCCTCAGC CTCGGTCCTT CTCAGCCGTC GGGATAGGAT3540
 CCAGGCATTT CTTTTAAATC TCAGAGGTAG CAGTAACTT TTCAGTATTG CTGTTAGCAA3600
 GTGTGTGTTT GCCAATAGAT ACCCATTATA CTAATGTGCC AAGTAAATGT TCATTGCACA3660
 TCTGCTTCCA CTGTGTTCCC ACGGGTGCCA TGAAGTGTGT GAGGAGCCCC TCATCTGGAG3720
 GGATGAGTGC TGCGTTGACT ACTGCTATCA GGATTGTGTT GTGTGGAATA TTCATCTACA3780
 TAAATTTTAT ATGCACAGTA ATTTCCCTTT TTATATGTCA AGTAACTATT TGTAAAAGTT3840
 ATACTCACAA ATTATTATAA TGATTACTAA TATATTTTTT CCATGTTTCA TTGCCTGAAT3900
 AAAAACTGTT TACCACTGTT AAAAAAAAAA AAAAAAAAAA AAAAAAATGG GAAAAAAAAG3960
 CTGGGGGGGG GGCCCCGTAG CC 3982

"BIBB" 04954959
 04954959

(2) INFORMATION ON SEQ ID NO. 402:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1876 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

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CTCTTGATC CCCTGGACCA CTGGGCATAC TCGCCATCCT CTTCCGGAGA TCTGGGCAGT 60
TCGCCTGCAT TAGAGCTCCT GATTGAGATT CAGTGCATCA GCCGTGCTAT CCATCACGTC 120
CACACCTCTG TGCCCACTCT TGAAGCTGTT GGGAAATATT CAGCAATGTC CGCATCAACT 180
TGCAGAAGAA TATAAATGAC ATTTCAAGGA TAGAAGATAC CTGATTTTTT TTCCTTTTAA 240
TTTTCTGGT GCCAATTTCA AGTTCCAAGT TGCTAATACA GCAACAATTT ATGAATTGAA 300
TTATCTTGGT TGAAAAATAA AAGATCACTT TCTCAGTTTT CATAAGTATT ATGTCTCTTC 360
TGAGCTATTT CATCTATTTT TGGCAGTCTG AATTTTTTAA ACCCATTTAA ATTTTTTTCC 420
TTACCTTTTT ATTTGCATGT GGATCAACCA TCGCTTTATT GGCTGAGATA TGAACATATT 480
GTTGAAAGGT AATTGAGAG AAATATGAAG AACTGAGGAG GAAAAAAGAA AAAAAAGAAA 540
GAACCAACAA CCTCAACTGC CTACTCCAAA ATGTTGGTCA TTTTATGTTA AGGGAAGAAT 600
TCCAGGGTAT GGCCATGGAG TGTACAAGTA TGTGGGCAGA TTTTCAGCAA ACTCTTTTCC 660
CACTGTTTAA GGAGTTAGTG GATTACTGCC ATTCACCTCA TAATCCAGTA GGATCCAGTG 720
ATCCTTACAA GTTAGAAAAC ATAATCTTCT GCCTTCTCAT GATCCAATA ATGCCTTACT 780
CTTCTTGAAA TTTTAACTTA TGATATTTTC TGTGCCTGAA TATTTGTTAT GTAGATAACA 840
AGACCTCAGT GCCTTCTGT TTTTCACATT TTCCTTTTCA AATAGGGTCT AACTCAGCAA 900
CTCGCTTTAG GTCAGCAGCC TCCCTGAAGA CCAAATTAG AATATCCATG ACCTAGTTTT 960
CCATGCGTGT TTCTGACTCT GAGCTACAGA GTCTGGTGAA GCTCACTTCT GGGCTTCATC 1020
TGGCAACATC TTTATCCGTA GTGGGTATGG TTGACACTAG CCCAATGAAA TGAATTAAAG 1080
TGGACCAATA GGGCTGAGCT CTCTGTGGGC TGGCAGTCCT GGAAGCCAGC TTTCCCTGCC 1140
TCTCATCAAC TGAATGAGGT CAGCATGTCT ATTCAGCTTC GTTTATTTTC AAGAATAATC 1200
ACGCTTTCCT GAATCCAAAC TAATCCATCA CCGGGGTGGT TTAGTGGCTC AACATTGTGT 1260
TCCCATTTC GCTGATCAGT GGGCCTCCAA GGAGGGGCTG TAAAATGGAG GCCATTGTGT 1320
GAGCCTATCA GAGTTGCTGC AAACCTGACC CTGCTCAGT AAAGCACTTG CAACCGTCTG 1380
TTATGCTGTG ACACATGGCC CCTCCCCCTG CCAGGAGCTT TGGACCTAAT CCAAGCATCC 1440
CTTTGCCAG AAAGAAGATG GGGGAGGAGG CAGTAATAAA AAGATTGAAG TATTTTGCTG 1500
GAATAAGTTC AAATCTTCT GAACCTCAAAC TGAGGAATTT CACCTGTAAA CCTGAGTCGT 1560
ACAGAAAGCT GCCTGGTATA TCCAAAAGCT TTTTATTCCT CCTGCTCATA TTGTGATTCT 1620
GCCTTTGGGG ACTTTTCTTA AACCTTCAGT TATGATTTTT TTTTCATACA CTTATTGGAA 1680
CTCTGCTTGA TTTTGGCCTC TTCCAGTCTT CCTGACACTT TAATTACCAA CCTGTTACCT 1740
ACTTTGACTT TTTGCATTTA AAACAGGACA CGGGGCAGGG AGAAAAGGGT TTTAGTTTTT 1800
AAACCCGGTG GTTACCATAA CGCGGGAAAA GGTGGCCCAT ACGGGGCAAA CGTTTTTTGA 1860
AGGTTAAGGG TATTTT

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1876

(2) INFORMATION ON SEQ ID NO. 403:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

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TCTGTTCTGT GGACAACTGT TACTGTTCTT CCGTGGCCAA CCATGGCGGC CACCAGCCCT 60
ACCCCCGCTC CGGCCACTTT CCCTGGACAG TGCCCTCGCA GGAGTACTCA CACCCGCTCC 120
CGCCACACC CTCCGTCCCC CAGTCCCTTC CCAGCCTGGC GGTCAGAGAC TGGCTTGACG 180
CCTCCCAGCA GCCCGGCCAC CAGGATTTCT ACAGGGTGTA TGGGCAGCCG TCCACCAAAC 240
ACTACGTGAC GAGCTAACGC CACGCAGGCG GCGGGGCGCT GGGGAATCTT CCTCCCCAGC 300
CCCCGGGCTC GGGAGTTATG CATCCAGAGA CCTGCCCTTC TACCTTCCTC GCCTCCCCCTC 360
TTECTCATTC CATTGCCCCA GGTCTTTTCC TTTTGGATTT TGTTTTGGTT TTGGCTTTGT 420
TTTTGATTTT TTTTATTAT GAATCTCCTG GACGCAGAGG TGACAGTGGG AGCTGGCCTG 480
GGCCAGGACG GCAGGTGGCC CTGGAGATGG GAAAGTGTCT GTGTGAGGC GCTGAGCTCT 540
CTCTCTGTTT CTCCTTTTTT CCTCTACTCC TTCCCCTTCA CACCCCCGTG GCTGGAAGGA 600
ACCTCGGCTT CCCTGAAAGC TTGGGGGTCC CACCCTTCTT ACCCCACCCG GGAGGAACGC 660
CCAGGGCCCC GGGCTTGTTT CTCCTCTTGT TTTCTTTTG GGCAGTTTGA TCACTGATCG 720
AGTAAGGAAT GACCTTTAGA TTGTGCGACT TTTGTTTTTG TTTTTTTAAA TTTTTTTAAA 780
CCAAGAATGA TTTCTCCTGC TTCCTTCTCC TCACCATCTT CCCAGACGGA GTTCAAAGGC 840
CACTTCTCAA GCAGCTTTTG GCACCTTCAG CCTCAGAGTG GAATCTTTTA AAGACAGGAC 900
CCCTATGTCC AGGAAAGGGG AAAAGGAACT TTGCCAATGA TAGTGACCAC AGCAAAAGCA 960
ATAAAATAAT AAAATAAAAA ACAATAGCAC AGCCCTTGTT GAGGTCAGCA GGGAGGAGGG1020
GCTGCCCCGA GTTGGGTCCT TGCCTGGATT TTGACACAGC AACTTCCTGT AGTGAGCACT1080
TTGTATGAAT CGTGGACTTC CTGTTCTCAA GGCGCAGGTA TTTATTCTGT ATCTGTCTAG1140
AGCACACACC AAAATCCAAC CTTCTAATAA ACATGATGGC GCAGTCCCAA AAAAAAGAAA1200
CAGAAGAAGA AAAGGG

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1216

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 271 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

RPRAGASIST LAGLSLKEGE DQKEIKIEPA QAVDEVEPLP EDYYTRPVNL TEVTTLQQR 60
 LQPDFQPVCA SQLYPRHKHL LIKRSLRCRK CEHNLSKPEF NPTSIKFKIQ LVAVNYIPEV120
 RIMSIPNLRY MKESQVLLTL TNPVENLTHV TLFECEEGDP DDINSTAKVV VPPKELVLAG180
 KDAAAEYDEL AEPQDFQDDP DIIAFRKANK VGIFIKVTPQ REEGEVTVCF KMKHDFKNLA240
 APIRPIEESD QGTEVIWLTQ HVELSLGPLL P 271

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 133 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

DLKQDQGKQK ICIFLKSLSGH LLTILLQKTR CSWWSTLSSF ILENIIIEIKV SNPTPGYQVK 60
 TASLLLGQNC GLLAEIFYGL QSKWSYLTHH MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFK120
 SMERMLVENI LKI 133

(2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

RGPGHLLKPN GGPPMKLGYG RNLDISPRLP LNRETVKRSI RFHREWPLIP NSFPHNSVFL60
 VSMKCLES HR KPVKIFLKKK KPQKTDHLSI QWTSI 95

(2) INFORMATION ON SEQ ID NO. 407:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

YLSLCPCWPG NFFQWCLLEE VFSSCHFKKI KLEIEYGWHD CTLLVLLFFY SSVPL 55

(2) INFORMATION ON SEQ ID NO. 408:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

(2) INFORMATION ON SEQ ID NO. 409:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

KGVGLLLIMGG QGQVLGHRER VRRMLQTPAH CPRSPLPAPA SDGAALIPCL SSLQIYEGAY60
HVLHKELPEV TNSVFHEINM WVSORTATAG TASPP 95

(2) INFORMATION ON SEQ ID NO. 410:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 296 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

VVRLAPTFGH	YVCTVISHAH	EVROMQELRR	VRSGVMSEKD	HMVTMHDVLD	AQWLYDNHKD	60
ESYLRRVVYP	LEKLLTSHKR	LVMKDSAVNA	ICYGAKIMLP	GVLRYEDGIE	VNQEIVVITT	120
KGEAICMAIA	LMTTAVISTC	DHGIVAKKIR	VIMERDTPYR	KWGLGPKASQ	KKLMIKQGLL	180
DKHGKPTSD	PATWKQEYVD	YSESAKKEVV	AEVVKAPQVV	AEAAKTAKSG	EESSESDET	240
PPAAPQLIKK	EKKKSQKDKK	AKAGLESAGE	PGDGSDTTK	KKKKKKKAKE	VELVSE	296

(2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 280 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

RDQGGGSLRS FPRLWTGRHD AVQGNMADAE VIILPKKHKK KKERKSLPEE DVAEIQHAAE 60
 FFIKPESKVA KLDTSQWPLL LKNFDKLNVR THTYPLACG SNPLKREIGD YIRTGFIND120
 KPSNPSSHEV VAWIRRLRV EKTGHSGTLD PKVTGCLIVC IERATRLVKS QQSAGKEYVG180
 IVRLHNAIEG GTQLSRALET LTGALFQRPP LIAAVKRQLR VRTIYESKMI EYDPERRLGI240
 FWVSCEAGTY IRTLCVHSDQ SRARGTSDAG ASEGSFWSHE 280

(2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 360 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

RHPHPEGVMG FSRGCGSASS ILWKPDHCPW QRFPGHQEFE EERLRPAGMH GTQRGRGGQV 60
 DPAAHCPGAH GETHLPRPDQ REDHGHGGAT TFSLNCSAAG TPTPSLVWVL PNGTDLQSGQ120
 QLQRFYHKAD GMLHISGLSS VDAGAYRCVA RNAAGHTERL VSLKVGLKPE ANKQYHNLVS180
 IINGETLKL PTPPGAGQGR FSWTLPNGMH LEGPQTLGRV SLLDNGTLTV REASVFDRT240
 YVCRMETEY PSVTSIPVIV IAYPPRITSE PTFVIYTRPG NTVKLNCMAM GIPKADITWE300
 LPDKSHLKAG VQARLYGNRF LHPQGSLLTIQ HATQRDAGFY KCMAKNILGS DSKTTYIHVF360

(2) INFORMATION ON SEQ ID NO. 413:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```

EEGDYTCFAE NQVGKDEMRV RVKVVITAPAT IRNKTYLAVQ VPYGDVVTVV CEAKGEPMPK 60
VTWLSPTNKV IPTSSEKYQI YQDGTLLIQK AQRSDSGNYT CLVRNSAGED RKTVWIHVNV120
QPPKINGNPN PITTVREIAA GGSRK LIECK AEGIPTPRVL WAFPEGVVLV APYYGNRITV180
HGNGSLDIRS LRKSDSVQLV CMARNEGGEA RLILQLTVLE PMEKPFIHDP ISEKITAMAG240
PQHSASTALP RGP RHPAWCG SFPMAPICRV DSSCSASTTR LTACYTLAVS PRWTLGPTAA300
WPAMPLATRR GWSP
314

```

(2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

```

RPVPAKLNPR SWPRTAGALP LRPPPLTMAV FHDEVEIEDF QYDEDSETYF YPCPCGDNFS 60
ITKEDLENCE DVATCPSCSL IIKVIYDKDQ FVCGETVPAP SANKELVKC
109

```

(2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

LILMGRLIYN XNYLFYKXDS IHXGRALEVQ YTRXFISSLH YDCEFPYKLX TXHXKGNXKI60
 HFYIHKNKTX PXET 74

(2) INFORMATION ON SEQ ID NO. 418:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 121 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

YPFFTLQCQRN RVFDISSYVK EMLQNVNCFK LKLPLKRPRY IYLVYIMFN ICQSILQVCS 60
 FISIKYGYV AQLLKWYICV YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMS120
 I 121

(2) INFORMATION ON SEQ ID NO. 419:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

FFFFFFFFFS FQRIHFFFFFF FFFFFFFGKNVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60
 YYKYNIQFKK TYGETQLMFF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

(2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 765 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```
IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTPNFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEIVDWWSK FDASSGEHEK CGQYIQKGY180
KLKIYNCELE NVAEFEGGLTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
TLNPVFGRMY ELSCYLPQEK DLKISVYDYG TFTRDEKVGE TIIDLENRFL SRFGSHCGIP360
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDGS RIRYGGRDYS LDEFEANKIL420
HQHLGAPEER LALHILRTQG LVPEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYYLRVVIWN TKDVILDEKS ITGEEMSDIY VKGWIPGNEE NKQKTDVHYR540
SLDGEENFNW RFVFPFDYLP AEQLCIVAKK EHFWSIDQTE FRIPPRLIQ IWDNDKFSLD600
DYLGFLELDL RHTIIPAKSP EKCRDMIPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
D GARVMAGKV EMTLEILNEK EADERPAGKG RDEPNMNPKL DLPNRPETSF LWFTNPCKTM720
KFIVWRRFKW VIIGLLFLLI LLLFVAVLLY SLPNYLSMKI VKPNV 765
```

(2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 289 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

```
ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120
CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180
PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240
NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNQVFFLR 289
```

(2) INFORMATION ON SEQ ID NO. 422:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

FFLYSFSSDN HDFSFKTIY LAFVSGGELA ISLLKPAIIV NLRTGLSWGGS EGKELFEQMC60
 VGGTGFHPTA KLVLLLEISFY NTKISLCQRF 90

(2) INFORMATION ON SEQ ID NO. 423:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

TPSGSSWRTY LSRRNSKGER TGPPLIPMTL PPGPLPTTCG NSQKINSSCN FSGDIAQTHI60
 TGDAHFFSIR DSQSEETPCV A 81

(2) INFORMATION ON SEQ ID NO. 424:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

ENWASRYFQS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKVCWIKAI 60
YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLEH SWFFFFFLLQ DLAVTQDGVQ120
WHDHGSLQP 129

(2) INFORMATION ON SEQ ID NO. 425:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 122 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENPAAD SLFQRRSFER RVCYISFFTV 60
TLWRLKDLVV SCFLKITGIW RPKVPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFPDYIV120
LS 122

(2) INFORMATION ON SEQ ID NO. 426:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 105 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

RFKKSPQRQN HNMSRRNKKL LDIPGSFLYD SGLQVKFLSL SSEEFELIPA KYFNLFITAS 60
SPIFFLGKGM LGLGPKLLAG GGAMCHSITD GCKCFTEQGS GLQQL 105

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(2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EKYEELRRKK KKKKRTNNLN CLLQNVGHEM LREEFQGMAM ECTSMWADFQ QTLFPLFKEL60
VDYCHSLHNP VGSSDPYKLE NIIFCLLMIQ LMPYSS 96

(2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

RKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60
TWGNGMRKRG GEEGRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFG GRLPIHPVEI120
LVAGLLGGVK PVSDRQAGKG LGDGGCGRER V 151

(2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(A) ORGANISM: HUMAN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

LCPFWWAIPM HVFGYGDTPS PQSHCAIVSK KCIISLFIC LITNEFIPDA FIQITGIFLN 60
WTSIFIPEVC ANGGCHVDGG NEAKHTSNYK CCSKTVIHSG IQTARPGCYG DRGLVL 116

1992 04 22 15 55

Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising
 - a) a nucleic acid sequence, selected from the group Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, 391-403,
 - b) an allelic variation of the nucleic acid sequences named under a)
 or
 - c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).
2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-127 and 391-403, or a complementary or allelic variant thereof.
3. Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, characterized in that they are expressed elevated in normal bladder tissue.
4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.
5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.
6. A nucleic acid sequence according to claims 1 to 4, wherein it has % homology to a human nucleic acid sequence.
7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a

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sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is *E. coli*, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403, which can be obtained according to claim 19.

21. An antibody according to claim , wherein it is monoclonal.

22. An antibody according to claim , wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 as tools for finding active ingredients against the bladder tumor.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403.

36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7,
wherein the size of the fragment has a length of at least 300 to
3500 bp.

Abstract

Human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal bladder tissue, which code for gene products or portions thereof, and their use, are described.

In addition, the polypeptides that can be obtained by way of the sequences and their use are described.

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Systematic Gene Search in the Incyte LifeSeq Database

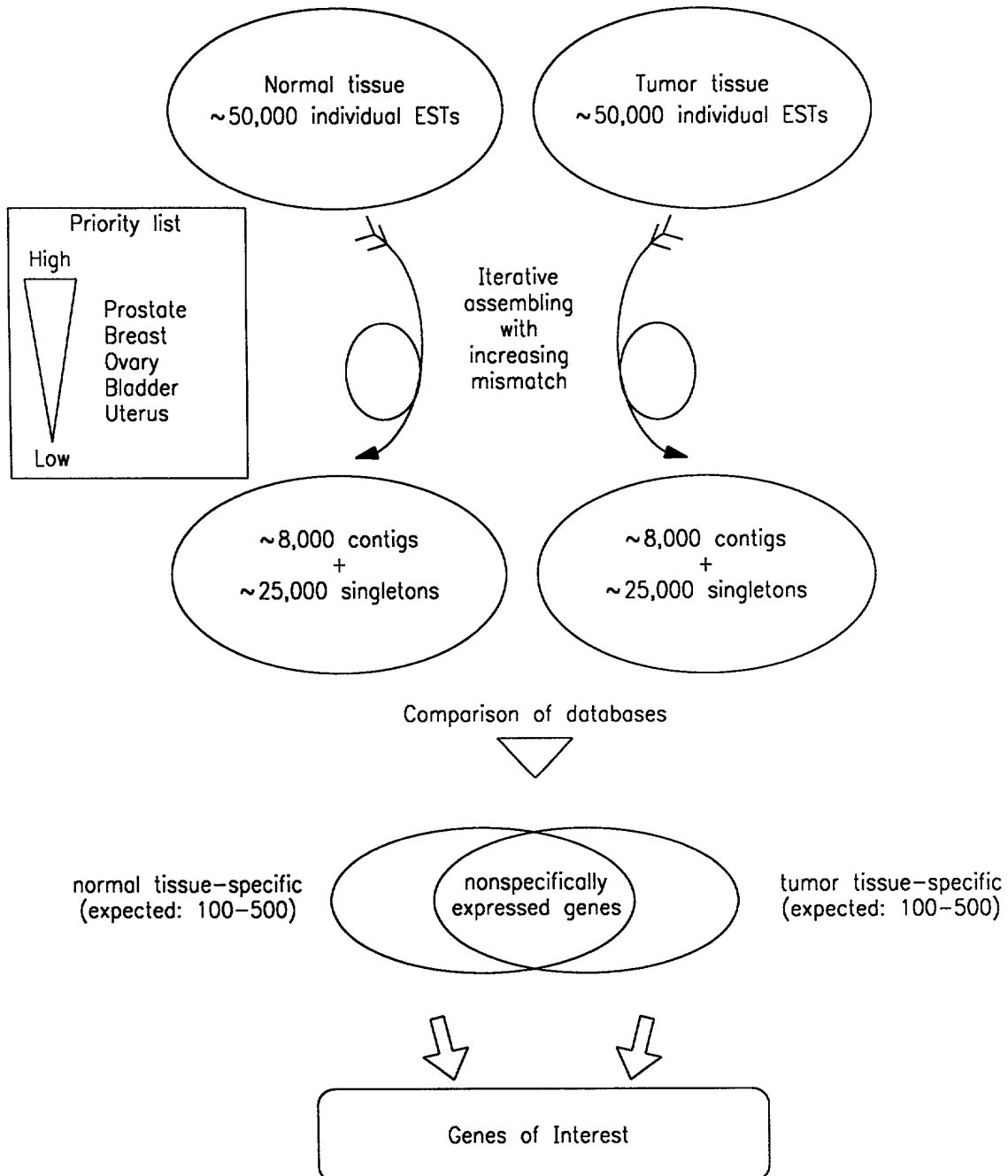
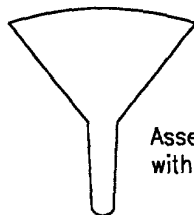


FIG. 1

Principle of EST Assembly

~50,000 ESTs per tissue

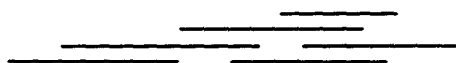


Assembly at 0% mismatch
with GAP4 (Staden)

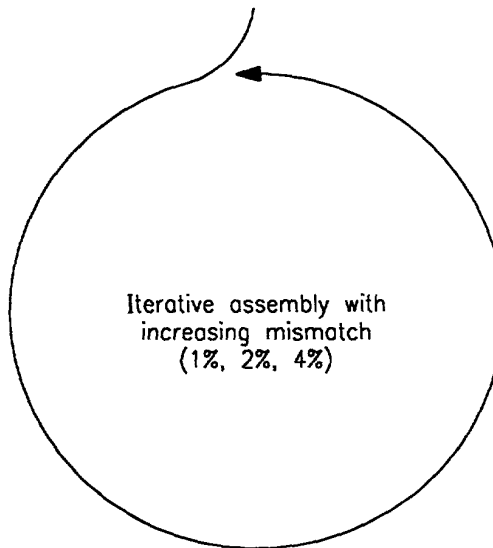


Contigs

Singletons



Contigs increasing in
number and length



Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs

~25,000 other singletons



~30,000 consensus-
sequences per tissue

FIG. 2a

~50,000 ESTs
of a tissue
(e.g.: uterus tumor)

GAP4 Assembly 1st Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 0

GAP4-Database 1:
Contigs 1 Singletons 1

unassembled
ESTs



GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 1



GAP4-Database 2:
Contigs 2 Singletons 2

unassembled
ESTs



GAP4 Assembly 3rd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2



GAP4-Database 3:
Contigs 3 Singletons 3

unassembled
ESTs

FIG. 2b-I

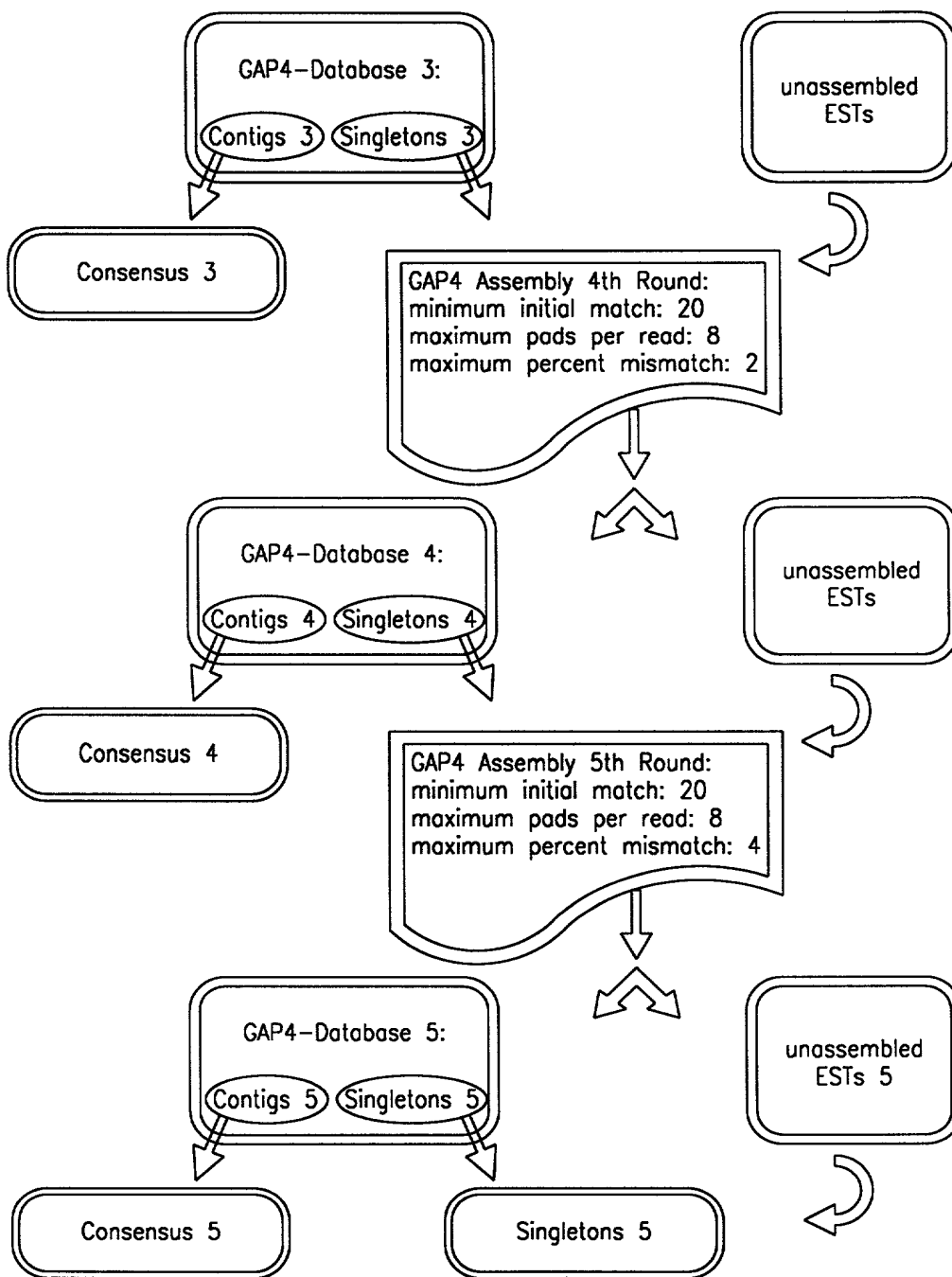


FIG. 2b-2

09573040.030504
T.09020" 040204950

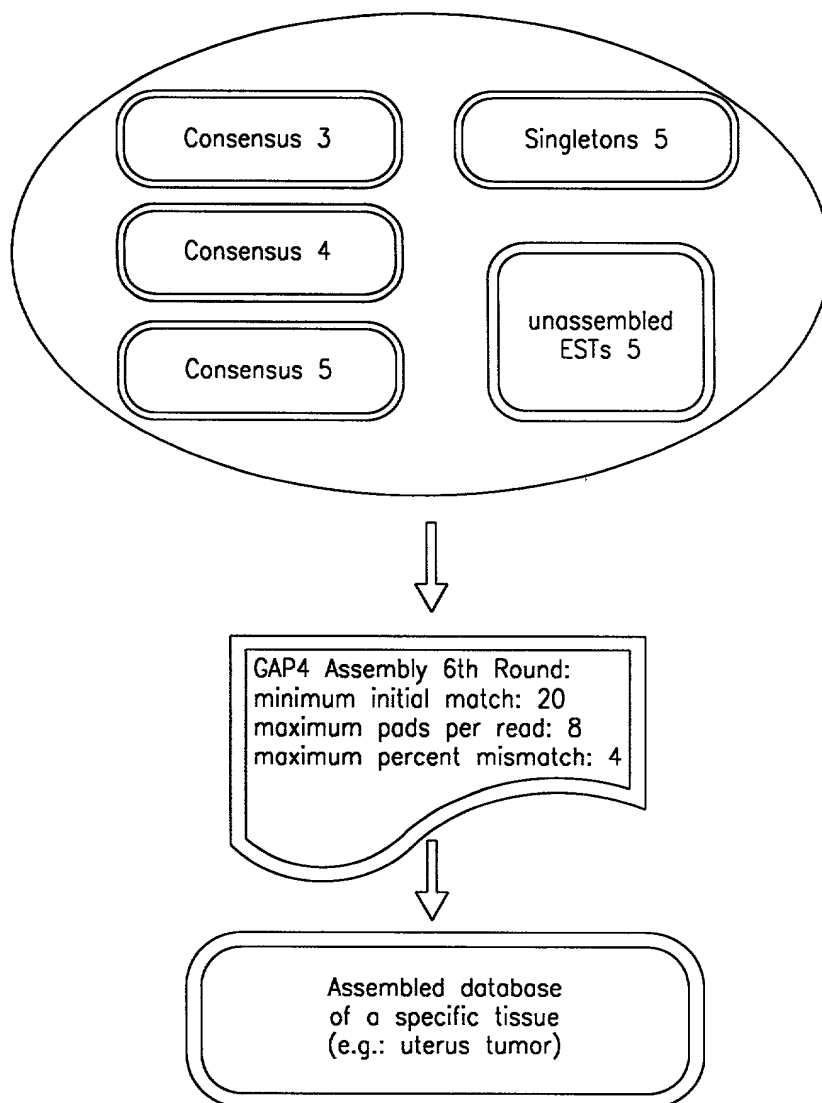


FIG. 2b-3

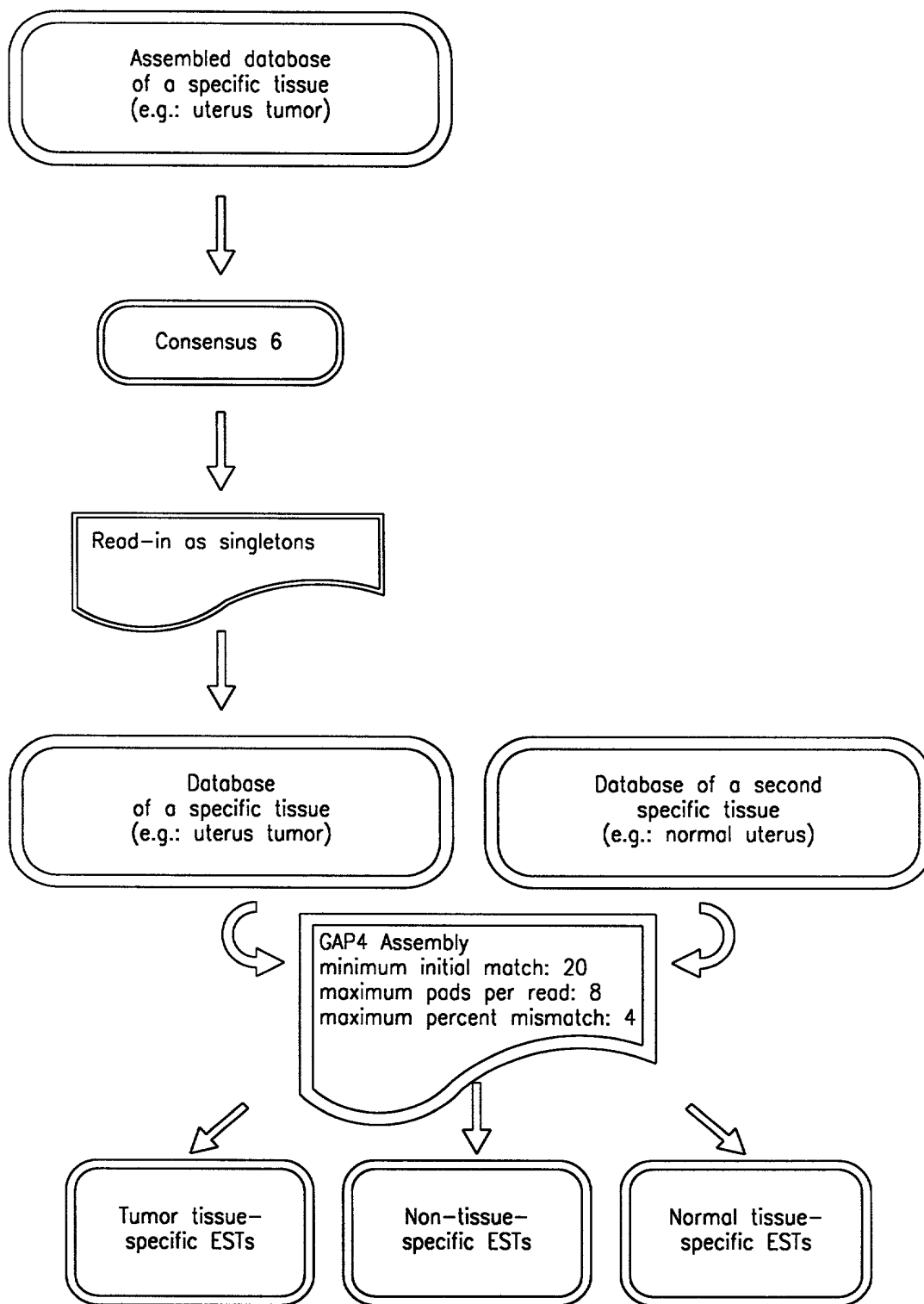


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue

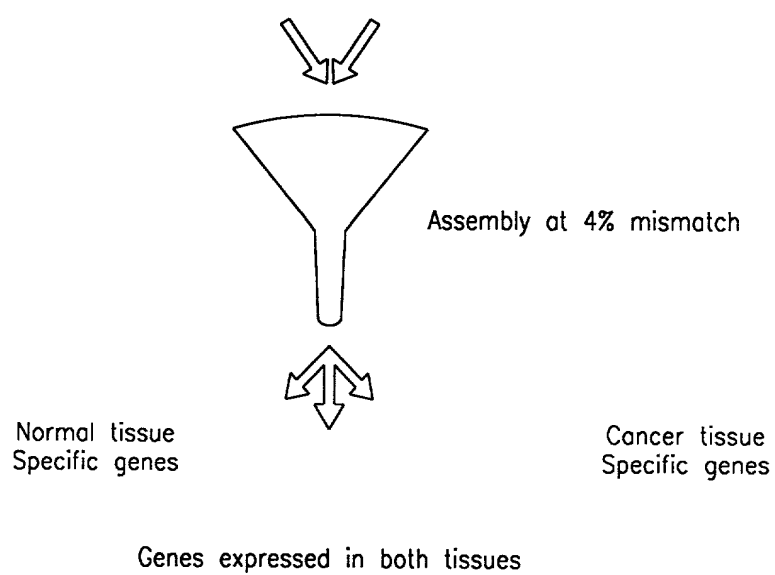


FIG. 3

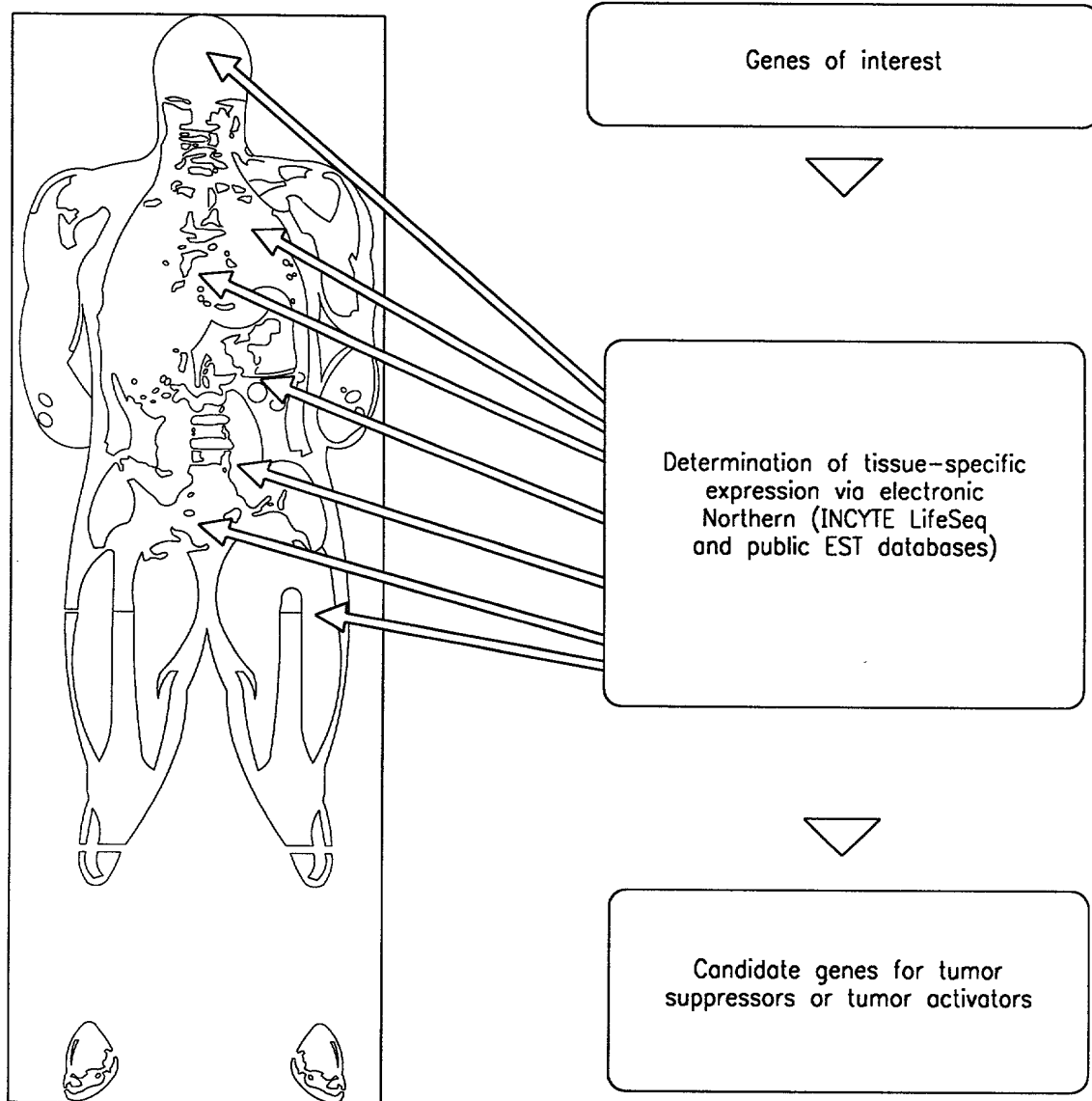


FIG. 4a

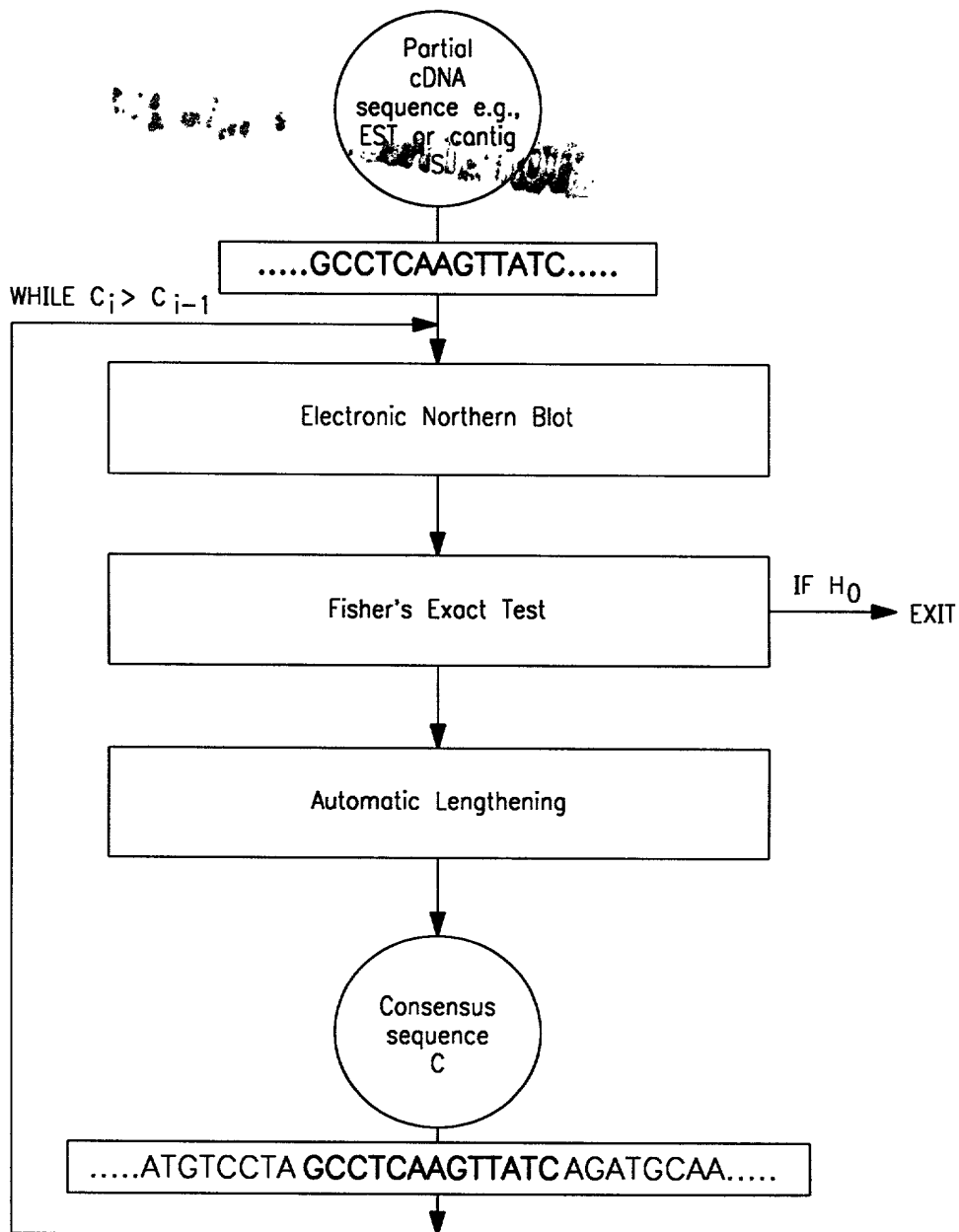


FIG. 4b

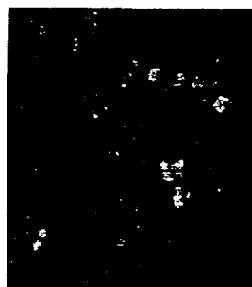
Isolation of genomic BAC and PAC clones



Chromosomal clone localization via FISH



Hybridization signal



Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes



Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

FIG. 5

Attorney Docket Number: SCH 1781**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01163 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 18 620.7	Germany	21 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

Declaration for Patent Application (Continued)

Correspondence Address:
MILLEN WHITE ZELANO & BRANIGAN, P.C.
~~Suite 1400~~
~~2200 Clarendon Boulevard~~
~~Arlington, VA 22201~~
 TEL (703) 243-6333
 FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of sole or first inventor (given name family name)

Thomas SPECHT

Signature

Date

Residence

Citizenship

Berlin, Germany

Germany

Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany

Full Name of additional joint inventor (given name family name)

Bernd HINZMANN

Signature

Date

Residence

Citizenship

Berlin, Germany

Germany

Post Office Address Parkstrasse 19, D-13127 Berlin, Germany

Full Name of additional joint inventor (given name family name)

Armin SCHMITT

Signature

Date

Residence

Citizenship

Berlin, Germany

Germany

Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany

Full Name of additional joint inventor (given name family name)

Christian PILARSKY

Signature

Date

Residence

Citizenship

Schönfeld-Weissig, Germany

Germany

Post Office Address Heinrich-Lange-Strasse 13c D-01474 Schönfeld-Weissig, Germany

Full Name of additional joint inventor (given name family name)

Edgar DAHL

Signature

Date

Residence

Citizenship

Potsdam, Germany

Germany

Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany

Full Name of additional joint inventor (given name family name)

André ROSENTHAL

Signature

Date

Residence

Citizenship

Berlin, Germany

Germany

Post Office Address Koppenplatz 10, D-10115 Berlin, Germany

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2-00
1-00

51587AWO MAXX24-P

Attorney Docket Number: SCH 1781

DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

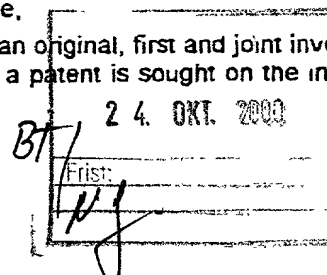
I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01163 and (if applicable) was amended on _____



I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

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 Suite 1400
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Berlin, Germany

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Germany

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Schönfeld-Weissig, Germany

Citizenship

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Date

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Potsdam, Germany

Citizenship

Germany

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Date

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Citizenship

Germany

Post Office Address Koppenplatz 10, D-10115 Berlin, Germany